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TITLE Mutations in the gene encoding peroxisomal alpha-methylacyl-CoA
racemase cause adult-onset sensory motor neuropathy
JOURNAL Nat. Genet. 24 (2), 188-191 (2000)
MEDLINE 20120722
PUBMED 10655068
REFERENCE 2 (bases 1 to 2005)
AUTHORS Ferdinandusse,S., Denis,S. and Wanders,R.J.A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Clinical Chemistry, Academic Medical
Center, Meibergdreef 9, Amsterdam 1105 AZ, The Netherlands
FEATURES
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/organism="Homo sapiens"
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66. .1214
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LOCUS AF047020
DEFINITION Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.
ACCESSION AF047020.1 GI:4204096
VERSION AF047020.1 GI:4204096
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS 1 (bases 1 to 2041)
TITLE Human alpha-methylacyl-CoA racemase cDNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2041)
AUTHORS Albers, C., Schmitz, W. and Conzelmann, E.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1998) Biozentrum, University of Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
REFERENCE 3 (bases 1 to 2041)
AUTHORS Albers, C., Schmitz, W. and Conzelmann, E.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Biozentrum, University of Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
REMARK
COMMENT Sequence update by submitter
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On Jan 29, 1999 this sequence version replaced gi:2896147.
Location/Qualifiers

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Matches 1998; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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LOCUS HSA130733 2068 bp mRNA linear PRI 30-NOV-2001
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ACCESSION AJ130733
VERSION AJ130733.1 GI:4995298
KEYWORDS 2-methylacyl-CoA racemase.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Amery,L., Fransen,M., De Nys,K., Mannaerts,G.P. and Van Veldhoven,P.P. Mitochondrial and peroxisomal targeting of 2-methylacyl-CoA racemase in humans.
JOURNAL J. Lipid Res. 41 (11), 1752-1759 (2000)
MEDLINE 20515663
PUBMED 11060344
REFERENCE 2 (bases 1 to 2068)
AUTHORS Van Veldhoven,P.P.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1999) Van Veldhoven P.P., Campus Gasthuisberg, Afdeling Farmakologie, Katholieke Universiteit Leuven, Herestraat, B-3000 Leuven, BELGIUM
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ORIGIN
Query Match 97.3%; Score 1950.8; DB 9; Length 2068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1985; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

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QY 1919 TTCTCCATGTGTTGATTTCTCTCAGGCTGTTAGCAAGTCTGATCTTATACCAACA 1978
Db 1942 TTCTCCATGTGTTGATTTCTCTCAGGCTGTTAGCAAGTCTGATCTTATACCAACA 2001
QY 1979 CACAGCAACATCCAGAAATAAAGTTCT 2005
Db 2002 CACAGCAACATCCAGAAATAAAGATCT 2028

RESULT 4
AK000912 1674 bp mRNA linear PRI 01-AUG-2002
LOCUS AK000912 Homo sapiens cDNA FLJ10050 fls, clone HEMBA1001257, highly similar
DEFINITION to Homo sapiens mRNA 2-methylacyl-CoA racemase.
ACCESSION AK000912
VERSION AK000912.1 GI:7021873
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
ORGANISM mRNA, clone_lib:HEMBA1 clone:HEMBA1001257.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1674)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

source Location/Qualifiers

1..1674

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/db_xref="taxon:9606"

/clone="HEMBA1001257"

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RESULT 5
BC009471

LOCUS 2946 bp mRNA linear PRI 12-JUL-2001

DEFINITION Homo sapiens, similar to alpha-methylacyl-CoA racemase, clone

ACCESSION MGC:3743 IMAGE:2958112, mRNA, complete cds.

BC009471

VERSION BC009471.1 GI:14495718

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2946)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (19-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guln, Letlicia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcleavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

FEATURES
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BASE COUNT 839 a 604 c 675 g 828 t

ORIGIN

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Best Local Similarity 91.6%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 2; Indels 161; Gaps 1;

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RESULT 6
AX106326
LOCUS AX106326 1621 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 107 from Patent WO0125272.
ACCESSION AX106326
VERSION AX106326.1 GI:13922012

KEYWORDS
SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1621)
TITLE Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.
Compositions and methods for therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0125272-A 107 12-APR-2001;

FEATURES CORIXA CORPORATION (US)
Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1322 CCACCTCTAATCAAGAAAAGATTACAGACTCTGATCTTACAGTATGATGATGATTTCTAAA 1381
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QY 1442 AGTTATCTGCTTCCAGCTTGTGATATTTGTTGATATTAAGATTCTGACTTATA 1501
Db 1381 AGTTATCTGCTTCCAGCTTGTGATATTTGTTGATATTAAGATTCTGACTTATA 1440
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QY 1562 ATTTACACTCTGATTTCTACAAATGTAGAAATGAGAAATGCCACAAATGTATGTGAT 1621
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Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 7
AX140617 1621 bp DNA linear PAT 31-MAY-2001
LOCUS Sequence 107 from Patent WO0134802.
DEFINITION AX140617
ACCESSION AX140617.1 GI:14280735
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolck,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 107 17-MAY-2001;
FEATURES CORIXA CORPORATION (US)
source Location/Qualifiers
1..1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN

Query Match 78.5%; Score 1574.2; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGGTCTGTGAGACTGTCCGGCCTGGCCCCGGCCGCTT 121
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QY 182 CCGCTACGAGTGAAGCCGCTTGGGCGGGGCAAGCGCTCGTATGTCTGAGCTGAAGCA 241
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QY 242 GCCCGGGGAGCCCGCTGCTGCGGGCTGTGTGCAAGCGGTGAGATGTGCTGTGAGCC 301
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Db 901 TTTTGAGGAGGTTGTTTCATCATGATCACAACAAGAAAGGCGGCTGTTATCACCAAGTGA 960
QY 1022 GGAGCAGAGCGTGAGCCCCCGCCCTGACACTCTGCTGTTAAACACCCAGCAGCATCCCTTC 1081
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Db 1261 CCACTCTAATCAAGAAAGAAATTACAGACTCTGATTCCTACAGTGATGATTGAATTCCTAAA 1320
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Db 1321 AATGTTATCATTAGGCTTTTGATTATTAAGAACTTGGGTACTTATACTAAATTTAGGT 1380
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QY 1622 AAAAGTCACGTGAACAGA 1640
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Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 8
AX200477 1621 bp DNA linear PAT 29-AUG-2001
LOCUS AX200477
DEFINITION Sequence 107 from Patent WO0151633.
ACCESSION AX200477
VERSION AX200477.1 GI:15390290
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kaijlos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 107 19-JUL-2001;
FEATURES CORIXA CORPORATION (US)
source Location/Qualifiers
1.1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN

Query Match 78.5%; Score 1574.2; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CGCCATGGCACTGCAGGGCATCTCGTGCTGAGCTGTCCGGCTGGCCCGGGCCCGCTT 121
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Db 1 CGCCATGGCACTGCAGGGCATCTCGGTATGAGCTGTCCGGCTGGCCCGGGCCCGCTT 60
QY 122 CTGTGCTATGTCCTTGGCTGACTTCGGGGCCCGGTGTGTACGCGTGAGACCGCCGGCTC 181
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Db 61 CTGTGCTATGTCCTTGGCTGACTTCGGGGCCCGGTGTGTACGCGTGAGACCGCCGGCTC 120
QY 182 CCGCTACGACGTAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTCTGACCTGAAGCA 241
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Db 961 GGAGCAGGACGTGAGCCCCCGCCCTGACACCTGTCTGTTAAACACCCCGACCTCCCTTC 1020
QY 1082 TTTCAAAGGATCCTTTCATAGGAGAACACACTGAGAGATACCTTGAAGATTGTGATT 1141
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Db 1201 TAGAGTACACATACATGTATGATGGAACATGAGACAGATTTACAGTGTCTTA 1260
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RESULT 10
AC008954
LOCUS AC008954 90111 bp DNA linear PRI 08-JUN-2001
DEFINITION Homo sapiens chromosome 5 clone CTD-2340N2, complete sequence.
AC008954
AC008954.6 GI:14329063
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 90111)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS 2 (bases 1 to 90111)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE
AUTHORS 3 (bases 1 to 90111)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS 4 (bases 1 to 90111)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
COMMENT On Jun 8, 2001 this sequence version replaced gi:13811891.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.1.
SFS Content:
SHGC-56588 G36925
WT-856 G02835
SHGC-36018 G30037.

FEATURES
Source 1. 90111
/organism="Homo sapiens"
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/clone="CTD-2340N2"
BASE COUNT 25692 a 18129 c 18543 g 27747 t
ORIGIN
Query Match 59.9%; Score 1201.4; DB 9; Length 90111;
Best Local Similarity 99.9%; Pred. No. 2.1e-263;
Matches 1202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 803 AGGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGA 862
Db 41636 AGGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGA 41695
QY 863 AATGAGAAGAAGTTTGCAGATGTATTTGCCAAGAAGACGACGACAGAGTGCTCAAT 922
Db 41696 AATGAGAAGAAGTTTGCAGATGTATTTGCCAAGAAGACGACGACAGAGTGCTCAAT 41755
QY 923 CTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTGACTTTTGAGGAGGTTGTCAATCA 982
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QY 1043 CCCGTGACCTCTGCTGTTAAACACCCCAAGCCATCCCTTTTCAAAAGGATCCTTCAT 1102
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QY 1163 GCTTAAGTCAAGTAAATCATTTGAAGTAAATGAAGTAAAGCTAGTCTCTAAGTTCCAGG 1222
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QY 2003 TCT 2005
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Db 42836 TCT 42838

RESULT 11
AC008971 131856 bp DNA linear PRI 30-NOV-2001
LOCUS AC008971
DEFINITION Homo sapiens chromosome 5 clone CTD-2376B17, complete sequence.
AC008971
VERSION AC008971.6 GI:17155029
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 131856)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 131856)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 131856)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 30, 2001 this sequence version replaced gi:7711381.
COMMENT
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 0.7.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 131.3kb). It is clipped at the overlap with AC008954.
The number of bases overlapped is 54595.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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BASE COUNT 37536 a 27071 c 27229 g 40020 t
ORIGIN

Query Match 59.9%; Score 1201.4; DB 9; Length 131856;
Best Local Similarity 99.9%; Pred. No. 2.3e-263;
Matches 1202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 6720 TGATTTATAAACTTTGGGTACTTATTAATAATATGTAGTTATCTGCTTCAGTTT 6779
QY 1463 GCTTGATATATTGTTGATATTAAGATTTCTGACTTATATTGTAATGGGTTCTAGTGAA 1522
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Db 6780 GCTTGATATATTGTTGATATTAAGATTTCTGACTTATATTGTAATGGGTTCTAGTGAA 6839
QY 1523 AAAGGAATGATATATTCTTGAAGACATCGATATACATTTATTACACTCTTGATCTACA 1582
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Db 6840 AAAGGAATGATATATTCTTGAAGACATCGATATACATTTATTACACTCTTGATCTACA 6899
QY 1583 ATGTAGAAAATGAGGAATGCGACAAATTTGATGTTGATATAAAGTCACGTGAACAGAGT 1642
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Db 6960 GATTGGTTGCATCCAGGCCCTTTTGTCTTGGTGTGATGATCTCCCTTAAGCACATTCCA 7019
QY 1703 AACTTTAGCAACAGTTATACACATTTGTAATTGCAAAAGAAAGTTTCACCTGTATTGAA 1762
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QY 1763 TCAGAAATGCGCTTCAACTGAAAAAACATATCCAAATATATGAGGAAATGTGTGCTCAC 1822
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Db 7080 TCAGAAATGCGCTTCAACTGAAAAAACATATCCAAATATATGAGGAAATGTGTGCTCAC 7139
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QY 1883 TGTTCCTCCCGTGGGTCTCTGGGTGTACAGCTTTCCTTCTCCATGTGTTGATTTCTCCT 1942
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QY 1943 CAGGCTGTAGCAAGTCTGTGATCTTATACCCACACACAGACATCCAGAAATAAGT 2002

QY 1823 TACGTAGAGTCCAGAGGGACAGTCAAGTTTATAGGCTTCCTGTATCCAGTAACTCGGGGCC 1882
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QY 1883 TGTTCCTCCCGTGGGCTCTGGGCTGTCCAGCTTTCCTTCTCCATGTTGTTGATTTCTCCT 1942
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QY 1943 CAGGCTGTAGCAAGTCTGTGATCTTATACCCACAACAGCAACATCCAGAAATAAAGT 2002
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Db 100218 CAGGCTGTAGCAAGTCTGTGATCTTATACCCACAACAGCAACATCCAGAAATAAAGA 100277
QY 2003 TCT 2005
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Db 100278 TCT 100280

RESULT 13
AX401900 1504 bp DNA linear PAT 06-JUN-2002
LOCUS Sequence 1576 from patent WO0210453.
DEFINITION AX401900
ACCESSION AX401900
VERSION AX401900.1 GI:21338080
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1.
AUTHORS Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
Elashoff,M.R.
TITLE Molecular toxicology modeling
JOURNAL Patent: WO 0210453-A 1576 07-FEB-2002;
Gene Logic, Inc. (US)
FEATURES
source 1.1504
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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BASE COUNT 375 a 367 c 408 g 354 t
ORIGIN

Query Match 41.4%; Score 830; DB 6; Length 1504;
Best Local Similarity 76.3%; Pred. No. 5.5e-179;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

QY 72 CTGCAGGGCATCTGCGTCTGTGAGCTGTCCGGGCTGGCCCCGGGCGGCTTCTGTGCTATG 131
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Db 2 CTGCGTGGCGTCAAGGCTTCTGAGCTGGCAGGCGCTGGCCCCAGGGCGTCTTCTGCGGATG 61
QY 132 GTCTGGCTGACTTCGGGGCGCGGTGTGTAGTACGCGGTGACCGGCCGCTCCCGCTACGAC 191
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Db 62 ATCTGGCGGACTTCGGCGCGCGAGGTGTGTGTGACAGACTGGGCTCGTGAACAC 121
QY 192 GTGAGCCGCTTGGGCGGCGGCAAGCGCTCGCTAGTGTGAGCTGAAGCAGCGCGGGA 251
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Db 122 CCCAGTCACTGGCGCGGAGGCAAGCGCTCGCTGGCGCTGACCTGAAGCGGTCTCCGGGA 181
QY 252 GCCCGCGTGTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTCCGGCG 311
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Db 182 GCCCGGCTGTGCGGCGCATGTGCGCACGCGCGAGCTGTGCTGAGCCCTTCCGTTGC 241
QY 312 GGTGTATGAGAACTCCAGCTGGGCCAGAGATCTGACGCGGAAATCCAAAGCTT 371
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Db 242 GGTGTATGAGAACTCCAGCTGGGCCAGAGACTTACGCGCAGGACAATCCAAAGCTC 301
QY 372 ATTATGCCAGGCTGAGTGTGATTTGGCCAGTACAGAAAGCTTCTGCCGTTAGCTGGCCAC 431
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Db 302 ATCTATGCCAGGCTGAGTGTGATTTGGCCAGTCTCGGAATTTCTCCAAGTAGCTGGCAAT 361
QY 432 GATATCAACTATTGGCTTGTGAGCTGTCTCTCAAAATTTGGCAGAGTGTGAGAAAT 491
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Db 362 GACATCAACTATATGCGCTTTGTACAGGTGTCTCTGTCAAAAGATTGGCAGGAGCGGTGAGAAC 421
QY 492 CCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTATGTGTGACTG 551
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Db 422 CCATACCTCCCGTAAACCTCCTGGCCGACTTGTGGCGGCTGAGCCCTCATGTGCACATTTG 481
QY 552 GGCATTTAATGAGCTTTTGTAGCCGACACGACACTGGCAAGGCTCAGTCAATGATGCA 611
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Db 482 GGCATTTTGTGCTGCTCTCTTGAAGCGCACGCGGTGCGCTAGGGCAGGTCAATGATGCG 541
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QY 672 CTGTGGAAGACACTTCGAGACAGACATGTTGATGCTGGAGCAGCTTCTTATAGCACT 731
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Db 602 CTGTGGGCACAGCCTCGAGGGCAAAACCTGTTAGATGGCGGGGCACCTTCTTACACAAAC 661
QY 732 TACAGACACAGCAGATGGGGAATTCATGGCTGTGAGCAATAGAACCCAGTCTTACGAG 791
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Db 662 TACAAGACCCGAGATGGGAGTTCATGGCTGTAGTGAATAGAACCCAGTCTTACACA 721
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Db 722 CTGCTGCTTAAAGCACTTGGACTTGAAGTCTGTGAAGAACTCCCAAGCAGATGAGCATAGAA 781
QY 852 GATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTGCAAAAGAACGAGGACAG 911
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Db 842 TGTGTCAAGATCTTGAACGGCACAGATGCTGTGTGACTCCGGTTCGACTTTTGAAGAG 901
QY 972 GTTGTTCATCATGATCACAACAAGAACGGGCTCGTTTATCACCACTGAGGAGCAGAC 1031
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Db 902 GCCCTCCACACACAGACACAAGAACGGGCTCGCTTCATCATGATGAGGAGCAGAT 961
QY 1032 GTGAGCCCCCGCCCTGACCTCTGTGTAAACACCCCAAGCATCCCTTCTTCAAAAG 1091
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Db 962 GATGCCCCCGCTGCTGCAACCCAGCTTTCAGAAACCCCTGCTGTCTTCTGCAAAAG 1021
QY 1092 GATCCTTTCATAGAGAACACACACTGAGAGATACTTGAAGAAATTTGATTCAGCCGGA 1151
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Db 1022 GACCTTCTGTGGGAGACACACACTGTGAAGGTGCTTAAAGACTATGATTCAGTCAGGAA 1081
QY 1152 GAGATTATCAGCTTAACCTCAGATTAATCATTTGAAGTAATAAGTAAAGCTAGTCTC 1211
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Db 1082 GAGATTCATCAGCTGCACTCGATGAATCATTTGAAGTAATAAGCTAAAGCCCAACCTC 1141
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QY 1272 CATACATTTGATGATGGAACACATGAGAGAACAGATTTACAGTGTCTACCACTTAAT 1331
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QY 1332 CAAGAAAGAAATTAAGACTCTGATTTCTACAGTGAATTTGAATTTGAATTTGAATTTGA 1391
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Db 1260 TCAAGACACAAGAAAGA--CTGATTAACAGAGAAATGACTGTGCTTCACACTGCTCATC 1317
QY 1392 ---ATTAGGCTTTGATTTATATAAATTTGGGTACTTATCTAAATTAATGTTAGTTAT 1448
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QY 1449 CTGCTTCCAGTTTGTGTATATAT 1474
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Db 1377 CTGCTTTCAGCTTACTTGTGAAGT 1402

RESULT 14
RN089905

LOCUS	KN089905	1504 bp	mRNA	linear	ROD 07-OCT-1997
DEFINITION	Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.				
ACCESSION	U89905				
VERSION	U89905.1				
KEYWORDS	GI:2145183				
SOURCE	Rattus norvegicus.				
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 1504) Schmitz,W., Fingerhut,R. and Conzelmann,E. Purification and properties of an alpha-methylacyl-CoA racemase from rat liver				
AUTHORS	Eur. J. Biochem. 222 (2), 313-323 (1994)				
TITLE	JOURNAL MEDLINE PUBMED 8020470				
REFERENCE	2 (bases 1 to 1504) Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E. Molecular cloning of cDNA species for rat and mouse liver alpha-methylacyl-CoA racemases				
AUTHORS	Biochem. J. 326 (Pt 3), 883-889 (1997)				
TITLE	JOURNAL MEDLINE PUBMED 97439733				
REFERENCE	3 (bases 1 to 1504) Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E. Direct Submission				
AUTHORS	Submitted (17-FEB-1997) Physiologic Chemistry II, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany				
TITLE	JOURNAL MEDLINE PUBMED 9307041				
REFERENCE	1. 1504 Location/Qualifiers				
AUTHORS	/organism="Rattus norvegicus"				
TITLE	/db_xref="taxon:10116"				
JOURNAL	/tissue_type="liver"				
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CDS	/note="required for bile acid synthesis and for catabolism of branched-chain fatty acids"				
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Query Match	41.4%; Score 830; DB 10; Length 1504;				
Best Local Similarity	76.3%; Pred. No. 5.5e-179;				
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QY	72	CTGCAGGCATCTCGGTCGTGAGAGCTGTCCGGCCTGGCCCCGGCCGCTCTGTGCTATG	131		
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QY	132	GTCCTGGCTGACTTCGGGGCGCGGTGTGTGTACGGCGGTGACCGGGCCCGGCTCCGCTACGAC	191		
Db	62	ATCCTGGCGGACTTCGGCGCGAGGTGTGTGCTCTGTGACAGACTGGGCTCCGTGAACAC	121		
QY	192	GTGAGCCGCTTGGGGCGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCGGGGGA	251		
Db	122	CCCAGTCACCTGGCCCCGAGGCAAGCGCTCGTGGCGCTGACCTGAAGCGGTCTCCGGGA	181		
QY	252	GCCGGCGTGTGCGGGCGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTCGCGCGC	311		
Db	182	GCCGGGTGTGCGGGCGATGTGCGCAGCGCGCGGACGTCGTGTGAGCCCTTCGCTGC	241		

QY	312	GGGTGCATGGAGAAACTCCAGCTGGGCCAGAGATTCGACCGGGAAATCCAAAGCCTT	371
Db	242	GGTGTCAATGGAGAAACTCCAGCTTGGGCCAGAGACTCTACGGCAGGAACAATCCAAAGCTC	301
QY	372	ATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTCTGCCGTTAGCTGGCCAC	431
Db	302	ATCTATGCCAGGCTGAGTGGATTGGCCAGTCGGAATTTCTCCAAAGTAGCTGGCCAT	361
QY	432	GATATCAACTATTTGGCTTTGTCCAGGTGTTCTCTCAAAAAATTGGCAGAAGTGGTGAAT	491
Db	362	GACATCAACTATGTGGCTTTGTCCAGGTGTCTCTCAAAAGATTGGCAGAGCGGTGAGAAC	421
QY	492	CCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTATGTGTGACATG	551
Db	422	CCATATCCCCCTCCCTGAACCTCCTGGCCGCACTTTGGTGGCGGTGGCCCTCATGTGCACATTG	481
QY	552	GGCATTTAATGGCTCTTTTGTACCCGCACACGCACTGGCAGAGGTCAGGTCAATTGATGCA	611
Db	482	GGCATTTTGTGGCTCTCTTCGAACGCACGCGGTCTGGCCCTTAGGGCAGGTCAATTGATGCG	541
QY	612	AATATGGTGAAGGAACAGCATTTTAAGTCTTTCTGTGSAAAAACTCAGAAATCGAGT	671
Db	542	AACATGGTGAAGGAACCGCATCTTAAGTACTTTCTGTGSAAAAACTCAGGCCATGGGT	601
QY	672	CTGTGGGAAGCACCCTCGAGGACAGAACATGTTGGATGGTGAAGCACCCTTCTATACGACT	731
Db	602	CTGTGGGCACAGCCTCGAGGGCAAAACCTGTTAGATGGCGGGCACCTTCTACACAACC	661
QY	732	TACAGGACAGCAGATGGGGAATTCAATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAG	791
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QY	792	CTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCAAATCAGATGAGCATGAT	851
Db	722	CTGCTGCTTAAAGACTTGGACTGAGTCTGAGGAACCTCCCAAGCAGATGAGCATAGAA	781
QY	852	GATTGGCCAGAAATGAAGTAAGAGTTTGCAGATGTATTGGCAAGAAGAAGCAGAGCAGAG	911
Db	782	GATTGGCCAGAAATGAAGTAAGATTTGCAGATGTGTTGCAAGAAGAAGCTAAGGCAGAG	841
QY	912	TGGTGTCAAAATCTTTGACGGGCACAGATGCCCTGTGTGACTGCCGTTCTGACTTTTGAAGAG	971
Db	842	TGGTGTCCAGATCTTTGACGGGCACAGATGCATGTGTGACCCCACTGCTGACTCTTGAAGAG	901
QY	972	GTTGTTCAATCATGATCACACAAAGGAACGGGGCTCGTTTATCAACCAGTGAGAGCAGAGAC	1031
Db	902	GCCCTCCACCACCAGCACAAACAGAGAACGGGGCTCCTTCATCACTGATGAGAGCAGCAT	961
QY	1032	GTTGAGCCCCCGCCCTGCACCTCTGCTTTAAACACCCCAAGCCATCCCTTCTTCAAAAGG	1091
Db	962	GCATGCCCCCGTCTGACCCCAAGCTTTCAGAAACCCCTGCTGTTCTCTGCAAAAGG	1021
QY	1092	GATCCTTTTCATAGGAGAAACACATGAGGAGATACCTTGAAAGATTGGATTCAGCCGCGAA	1151
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QY	1152	GAGATTTCATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAAGTTAAAGCTAGTCTC	1211
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QY	1212	TAACTTCCAGGCCACGGCTCAAGTGAATTTGAATACTTCATTTACAGTGTAGAGTAACA	1271
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QY	1272	CATAACATTTGATGATGAAACATGGAGGAACAGTATTACAGTGTCTACACACTCTAAT	1331
Db	1200	CCCACCACTGTCCGTATGAAATGTGAATGAACAGTAATGAAGTAATCCAAATATTCCAA	1259
QY	1332	CAAGAAAAGATTTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAAAATGGTTATC	1391
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Db 1318 CGAGCCTCTGATTCAGAGAGATATTTTGTGTGCTACTGATATATTAAGTGTGGCAGTT-TT 1376

QY 1449 CTGCTTCAGATTGCTTGATATATT 1474
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RESULT 15
RN2ARYLCO 1498 bp mRNA linear ROD 15-SEP-1997
LOCUS RN2ARYLCO 1498 bp mRNA linear ROD 15-SEP-1997
DEFINITION R.norvegicus mRNA for 2-arylproplyl-CoA epimerase.
ACCESSION Y08172
VERSION Y08172.1 GI:1552373
KEYWORDS 2-arylproplyl-CoA epimerase; epimerase.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Reichel,C., Brugger,R., Bang,H., Gelslinger,G. and Brune,K.
TITLE Molecular cloning and expression of a 2-arylproplyl-coenzyme A
JOURNAL Mol. Pharmacol. 51 (4), 576-582 (1997)
MEDLINE 97260501
PUBMED 9106621
REFERENCE 2 (bases 1 to 1498)
AUTHORS Reichel,C.
TITLE Direct Submission
REFERENCE Submitted (02-AUG-1996) C. Reichel, University Erlangen/Nuernberg,
JOURNAL Dept. Exp./Clin. Pharmacology, Universitaetsstr. 22, D-91054
          Erlangen, FRG

FEATURES
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Query Match 40.2%; Score 807; DB 10; Length 1498;
Best Local Similarity 75.7%; Pred. No. 1e-173;
Matches 1053; Conservative 0; Mismatches 330; Indels 8; Gaps 4;

QY 87 GTCGTGAGAGCTGTCCGGCCTGGCCCCGGGGCCGCTTCTGTGCTATGCTCTGGCTACTTC 146
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Db 7 GTCAGGGTTCTGGCAGGCCCTGGCCCCAGGGCCGCTTCTGCGGATGATCTCGCGGACTTC 66

QY 147 GGGCGCGTGTGTACCGCTGGACCGGCCCGGCTCCCGCTACGAGTGAGCCGCTTGGGC 206
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Db 67 GGGCGCGAGGTGTGCTCTGTGACAGACTGGCTCGTGAACCAACCCAGTCAACCTGGCC 126

QY 207 CGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGACAGCCGGGGAGCCCGCGTGTGCGG 266

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Db	127	CGAGCGAAGCGCTGCGCTGGCGCTGGACCTGAACCGGCTCTCCGGAGAGCCGGCGTGTGGCG	186
QY	267	CGTCTGTGCAAGCGGTGGATGTGCTGCTGTGAGCCCCCTCCGCCGGGTGTATGGAGAAA	326
Db	187	CGCATGTTCTCACC GCCCGGACGCTGTGCTGGAGCCCCCTCCGTTGGGTGTATGGAGAAA	246
QY	327	CTCCAGCTGGGCCCAAGATTTCTGCAAGCGCGGAAAAATCCAAAGCTTATTATGCGAGGCTG	386
Db	247	CTCCAGCTTGGGCCAGAGACTCTACGGCAGACAAATCCAAAGCTCATCTATGCGAGGCTG	306
QY	387	AGTGGATTTGGCCACTCAGGAAGCTTCTGCGGTTATAGCTGGCCACGATATCACTATTTG	446
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QY	447	GCTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGATGCCCCGCTG	506
Db	367	GCTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGGTGAAGATCCGATGCCCCGCTG	426
QY	507	AATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTGTCACCTGGGCATTAATGGCT	566
Db	427	AACCTCTGGCGCGCACTTTGGTGGGCTGGCTCTCATGTGACATTTGGGCACTTTGGTGGCT	486
QY	567	CTTTTTCACCGCACACGCACTGGCAGGGTCAAGTCAATTTGATGCAAAATATGTTGAAGA	626
Db	487	CTCTTTCGAACGCAAGCGGCTGTGGCTTAGGGCAGGTCATTGATGCCAATGTTGAAGA	546
QY	627	ACAGCATATTTAAGTCTTTCTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACC	686
Db	547	ACGCGATACTTAAGTACTTTCTCTGTGGAAACTCAGGCAATCGGCTCTGTGGGCAAGCCT	606
QY	687	CGAGGACAGAACATGTTGGATGTTGAGAGCAGCACCCTTCTATACGACTTACAGACAGCAGAT	746
Db	607	CGAGGCAAAACCTGTAGATGCGGGGCACTTTCTACACAACTTACAAAGCCGAGAT	666
QY	747	GGGCAATTCATGCTGTGGAGCAATAGAACCCAGTCTTACAGCTGCTGATCAAGA	806
Db	667	GGGAGTTTCATGCTGTAGGTGCAATAGAACCCAGTCTTACACACTGCTGCTTAAAGA	726
QY	807	CTTGGACTAAGCTGTGATGAACCTCCCAATCAGATGAGCATGATGATTTGCCAGAAATG	866
Db	727	CTTGGACTGTGATGTGAGGAACCTCCAGCCAGATGAGCATGAAAGATTGGCCAGAAATG	786
QY	867	AAGAGCAAGTTTGCATGTATTTGCCAAAGAACGAAAGCAGAGTGGTGTCAATCTTT	926
Db	787	AAGAGCAATTTTGCATGTATTTGCCAAAGAACGAAAGCAGAGTGGTGTCCAGATCTTT	846
QY	927	GACGGCAGATGCTGTGTGATGCTCCGGTCTGACTTTTGAGAGGTTGTCTACATGAT	986
Db	847	GACGGCAGATGATGTGTGACCCAGTGTGACTCTTGAGAGGCCCCCTCCACACACAG	906
QY	987	CACAACAAGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTGAGCCCCCGCCT	1046
Db	907	CACAACAAGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGATGATTTCCCGGCTCT	966
QY	1047	GCACCTGTGCTTAAACACCCAGCCATCCCTTTTCAAAAAGGATCTTTCATAGGA	1106
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QY	1107	GAACAACACTGAGAGATACTTGAAGAAATTTGGATTACGCCGCAAGAGATTTATCAGCTT	1166
Db	1027	GAGCACACTGTAGAGTGTCTTAAAGACTATGATTTCAAGTCAAGAGAGATCCACCAAGCTG	1086
QY	1167	AACCTGATTAATATCTGAAGATTAAGTAAAGCTAGTCTTAACCTCCAGGCCCCA	1226
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Db	1145	CAGCTCAAGTGAATCTGAAGGCTGTATCTGTACTGGAGAAAGATGCCACCACTGTCCGT	1204
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:27:38 ; Search time 3418 Seconds

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Title: US-09-967-305-3

Perfect score: 1146

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens alpha-methylacyl-CoA racemase (RM) mRNA, complete cds.
ACCESSION AF158378
VERSION AF158378.1 GI:6653127
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2005)
Ferdinandusse,S., Denis,S., Clayton,P.T., Graham,A., Rees,J.E.,
Allen,J.T., McLean,B.N., Brown,A.Y., Vreken,P., Waterham,H.R. and
Wanders,R.J.

TITLE Mutations in the gene encoding peroxisomal alpha-methylacyl-CoA
JOURNAL racemase cause adult-onset sensory motor neuropathy
MEDLINE Nat. Genet. 24 (2), 188-191 (2000)
PUBMED 20120722
10655068
REFERENCE 2 (bases 1 to 2005)
AUTHORS Ferdinandusse,S., Denis,S. and Wanders,R.J.A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Clinical Chemistry, Academic Medical
Center, Meibergdreef 9, Amsterdam 1105 AZ, The Netherlands
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source location/Qualifiers
1. 2005
/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 3.1e-249;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX106326
DEFINITION Sequence 107 from Patent WO0125272.
ACCESSION AX106326
VERSION AX106326.1 GI:13922012
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;

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REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Skelky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 107 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1. 1621
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 461 a 330 c 412 g 418 t
ORIGIN

Query Match 99.7%; Score 1142.8; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 1.6e-248;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 107 from Patent WO0134802.
ACCESSION AX140617
VERSION AX140617.1 GI:14280735
KEYWORDS
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1621)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skelky,Y.A. and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 107 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%; Pred. No. 1.6e-248;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 107 from Patent WO0151633.

ACCESSION AX200477

VERSION AX200477.1 GI:15390290

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1621)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0151633-A 107 19-JUL-2001;

FEATURES

source CORIXA CORPORATION (US)

location/Qualifiers

1. 1621

/organism="Homo sapiens"

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BASE COUNT 461 a 330 c 412 g 418 t

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Best Local Similarity 99.8%; Pred. No. 1.6e-248;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 REFERENCE 1
 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
 Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
 Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A., Hepler, W.T.
 and Henderson, R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate
 cancer
 JOURNAL Patent: WO 0173032-A 107 04-OCT-2001;
 CORIXA CORPORATION (US)
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 ACCESSION AK000912

VERSION AK000912.1 GI:7021873
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SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone_lib:HEMBA1 clone:HEMBA1001257.
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REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Tojiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1674)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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REFERENCE 1 (bases 1 to 2041)
AUTHORS Albers,C., Schmitz,W. and Conzelmann,E.
TITLE Human alpha-methylacyl-CoA racemase cDNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2041)
AUTHORS Albers,C., Schmitz,W. and Conzelmann,E.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1998) Biozentrum, University of Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
REFERENCE 3 (bases 1 to 2041)

AUTHORS Albers, C., Schmitz, W. and Conzelmann, E.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Biozentrum, University of Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
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COMMENT On Jan 29, 1999 this sequence version replaced gi:2896147.
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VERSION AJ130733.1 GI:4995298
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REFERENCE
1
AUTHORS Amerly, L., Fransen, M., De Nys, K., Mannaerts, G.P. and Van
Veldhoven, P.P.
TITLE Mitochondrial and peroxisomal targeting of 2-methylacyl-CoA
racemase in humans
JOURNAL J. Lipid Res. 41 (11), 1752-1759 (2000)
MEDLINE 20515663
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REFERENCE
2 (bases 1 to 2068)
AUTHORS Van Veldhoven, P.P.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1999) Van Veldhoven P.P., Campus Gasthuisberg,
Afdeling Farmakologie, Katholieke Universiteit Leuven, Herestraat,
B-3000 Leuven, BELGIUM
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QY 779 GCATGATGATGGCCGAATGAGAAGAAGTTGCAGATGTATTGGCAAGAGACGA 838
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Db 867 GCACGGATGATTTGGCCAGAAATGAGAAGAAGTTTGAGATGTATTGGCAAGAGACGA 926
QY 839 AGCGAGAGTGTGTCAATCTTTGACGGGCACAGATGCTGTGACTCCGGTCTGACTT 898
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Db 927 AGCGAGAGTGTGTCAATCTTTGACGGGCACAGATGCTGTGACTCCGGTCTGACTT 986
QY 899 TTGAGGAGGTTGTTCAATCATGATCACAACAAGGAGCGGGCTCGTTATCACCAGTGAGG 958
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Db 987 TTGAGGAGGTTGTTCAATCATGATCACAACAAGGAGCGGGCTCGTTATCACCAGTGAGG 1046
QY 959 AGCAGGACGTGAGCCCCCGCTGCACCTGTGCTTTAAACACCCAGCCATCCCTCTT 1018
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Db 1047 AGCAGGACGTGAGCCCCCGCTGCACCTGTGCTTTAAACACCCAGCCATCCCTCTT 1106
QY 1019 TCAAAAGGATCTTTTATAGGAGAACAACACTGAGAGATACCTGAAGAATTGGATTCA 1078
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Db 1107 CCAAGAGGATCTTTTATAGGAGAACAACACTGAGAGATACCTGAAGAATTGGATTCA 1166
QY 1079 GCCCGGAAGAGATTATACAGCTTAACCTCAGATAAATCATTTGAAGTAAATGAAG 1138
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Db 1167 GCCGAGAAGAGATTATACAGCTTAACCTCAGATAAATCATTTGAAGTAAATGAAG 1226
QY 1139 CTAGTCTC 1146
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Db 1227 CTAGTCTC 1234

RESULT 9
BC009471      2946 bp      mRNA      linear      PRI 12-JUL-2001
LOCUS
DEFINITION
Homo sapiens, similar to alpha-methylacyl-CoA racemase, clone
MGC:3743 IMAGE:2958112, mRNA, complete cds.
BC009471
BC009471.1 GI:14495718
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2946)
REFERENCE
AUTHORS
TITLE
JOURNAL
Strausberg, R.
Direct Submission
Submitted (19-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 9 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4204096.
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location/Qualifiers
1..2946
/organism="Homo sapiens"
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IYARLSGFQSGSFCRLAGHDINYLALSGRNSIFEKFSVENSEIESVSTSRTEHVG
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BASE COUNT      839 a      604 c      675 g      828 t
ORIGIN

Query Match      70.9%; Score 812.4; DB 9; Length 2946;
Best Local Similarity 85.9%; Pred. No. 1.4e-173;
Matches 984; Conservative 0; Mismatches 1; Indels 161; Gaps 1;

QY 1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCGTTCTGT 60
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Db 13 ATGGCACTGCAGGGCATCTCGGTCATGAGCTGTCCGGCCCTGGCCCCGGCCGTTCTGT 72

QY 61 GCTATGCTCTGCTGCTGACTTCCGGGGCGCGTGTGTACGCGTGGACCGCGCCGCTCCCGC 120
    |||||||
Db 73 GCTATGCTCTGCTGCTGACTTCCGGGGCGCGTGTGTACGCGTGGACCGCGCCGCTCCCGC 132

QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTGCTAGTGTGACCTGAAGCAGCCG 180
    |||||||
Db 133 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTGCTAGTGTGACCTGAAGCAGCCG 192

QY 181 CGGGGAGCCCGCGCTGCTGCGGCTGTGTGCAAGCGGTCGGATGCTGCTGAGCCCTTC 240
    |||||||
Db 193 CGGGGAGCCCGCGCTGCTGCGGCTGTGTGCAAGCGGTCGGATGCTGCTGAGCCCTTC 252

QY 241 CGCCCGCGGTGTCAATGAGAAATCCAGCTGGGCGGCAAGATTCGACGCGGAAATCCA 300
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Db 253 CGCCCGCGGTGTCAATGAGAAATCCAGCTGGGCGGCAAGATTCGACGCGGAAATCCA 312

QY 301 AGGCTTATTTATGCCAGGCTGAGTGTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
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Db 313 AGGCTTATTTATGCCAGGCTGAGTGTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 372

QY 361 GGGCAGCATATCACTATTGGCTTTGTCAAGGTCTCTCAAAAATTGGCAGAGTGTG 420
    |||||||
Db 373 GGGCAGCATATCACTATTGGCTTTGTCA----- 402

QY 421 GAGAATCCGATCCCGCCCGCTGATCTCTGCTGACTTGTGCTGTGGCTTATGTGT 480
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Db 403 ----- 402

QY 481 GCACTGGGCAATTAATGCTCTTTTGGACCGCACGACACTGGCAAGGTCAGGTCAATT 540
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Db 403 ----- 402

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Db 403 -----GGTGGAAAGGACAGCATATTTAAGTCTTTTCTGTGGAAACTCAGAAA 451

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTGGAGCAGCCTTCTAT 660
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Db 452 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTGGAGCAGCCTTCTAT 511

QY 661 ACGACTTACAGACAGCAGAGTGGGAATTCAATGCTGTTGGAGCAATAGAACCCAGTTC 720
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Db 512 ACGACTTACAGACAGCAGATGGGAATTCAATGCTGTTGGAGCAATAGAACCCAGTTC 571

QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
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Db 572 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 631
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QY 781 ATGATGATTTGGCCCAAAATGAAGAAGAGTTCGACATGTATTTGCCAAGAAGCAGAG 840
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QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGTTCTGACTTTT 900
    |||||||
Db 692 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGTTCTGACTTTT 751

QY 901 GAGGAGGTTGTTTCATCATGATCACACACAGGAACGGGGCTCGTTATTCACAGTAGAG 960
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Db 752 GAGGAGGTTGTTTCATCATGATCACACACAGGAACGGGGCTCGTTATTCACAGTAGAG 811

QY 961 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTCTTTC 1020
    |||||||
Db 812 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTCTTTC 871

QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGAATTTGATTACAGC 1080
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Db 872 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGAATTTGATTACAGC 931

QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATGAAGCT 1140
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Db 932 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATGAAGCT 991

QY 1141 AGTCTC 1146
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Db 992 AGTCTC 997

RESULT 10
AX401900      1504 bp      DNA      linear      PAT 06-JUN-2002
LOCUS      AX401900      Sequence 1576 from Patent WO0210453.
DEFINITION      AX401900
ACCESSION      AX401900
VERSION      AX401900.1 GI:21338080
KEYWORDS
SOURCE
ORGANISM      Norway rat.
                Rattus norvegicus.
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1
AUTHORS      Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
                Blashoff,M.R.
TITLE      Molecular toxicology modeling
JOURNAL      Patent: WO 0210453-A 1576 07-FEB-2002;
                Gene Logic, Inc. (US)
FEATURES
source      1..1504
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                /db_xref="taxon:10116"
                /note="EMBL/GenBank Accession No. NM_012816"
BASE COUNT      375 a      367 c      408 g      354 t
ORIGIN

Query Match      67.8%; Score 776.8; DB 6; Length 1504;
Best Local Similarity 80.1%; Pred. No. 1.5e-165;
Matches 913; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

QY 7 CTGAGGGCATCTCGGTCGTGAGCTGTCCGGCTGGCCCCCGGGCGTCTGTGCTATG 66
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Db 2 CTGCGTGGCGTCAAGGTTCTGTGAGCTGGCAGGCGCTGGCCCCCAGGGCGTTCTGCGGATG 61

QY 67 GTCTGGCTGACTTCGGGGCGCGGTGTGTACGCGTGGACCGCGCGGCTCCCGTACGAC 126
    |||||||
Db 62 ATCTGGCGGACTTCGGCGCGCGAGCTGTGTGTGAGACAGACTGGGCTCCGTAACAC 121

QY 127 GTGAGCCGCTTGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCGCGGGGA 186
    |||||
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QY 187 GCCCGGTGCTGCGGCGTCTGTGCAAGCGGTGGAATGTGCTGTGAGACCCCTTCGCGCCG 246
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QY	247	GGTGCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAAATCCAAGGCTT	306
Db	242	GGTGCATGGAGAACTCCAGCTGGGCCAGAGACTCTACGGCAGCAATCCAAGCTC	301
QY	307	ATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTCCGGTTAGTGGCCAC	366
Db	302	ATCTATGCCAGGCTGAGTGGATTGGCCAGTCGGGAATTTCTCCAAGTAGCTGGCCAT	361
QY	367	GATATCAACTATTTGGCTTTGTACAGGTGTTCTCTCAAAAAATTGCCAGAAGTGTGAGAA	426
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QY	427	CCGATGCCCCGCTGAATCTCCGTGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGACTG	486
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QY	487	GGCATTTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGGTCATGATGCA	546
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QY	547	AATATGCTGGAAGGAACAGCATATTTAAGTCTTTCTGTGGAATACTCAGAAATCGAGT	606
Db	542	AACATGGTGAAGGAACGGCATTAAGTACTTTCCTGTGGAATACTCAGGCCATGGGT	601
QY	607	CTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGGTGGACACCTTCTATACGACT	666
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QY	667	TACAGGACAGCAGATGGGAATTCATGCGCTGTTGGAGCAATAGAACCCAGTTCACGAG	726
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QY	727	CTGCTGATCAAAAGACTTGACTTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGAT	786
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QY	787	GATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAGAAGACGAAGGCAGAG	846
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Db	902	GCCCTCCACCAACAGCACAAGAACGGGGCTCCTTCATCACTGATGAGGAGCAGCAT	961
QY	967	GTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAAG	1026
Db	962	GCATGCCCCCGCTCTGCACCCCAAGCTTTCAGAACCCCTGCTGTTCTTCTGCAAAAG	1021
QY	1027	GATCCTTTTCATAGAGAGAACACACTGAGAGATACTTGAAGAAATTGGATTTCAGCCGGA	1086
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QY	1087	GAGATTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGTTAAAGCTAGTCTC	1146
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LOCUS	RNU89905	1504 bp	mRNA linear ROD 07-OCT-1997
DEFINITION	Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.		
ACCESSION	U89905		
VERSION	U89905.1	GI:2145183	
KEYWORDS			
SOURCE	Rattus norvegicus.		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	1 (bases 1 to 1504)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratus.
AUTHORS	Schmitz,W., Fingerhut,R. and Conzelmann,E.	
TITLE	Purification and properties of an alpha-methylacyl-CoA racemase from rat liver	
JOURNAL	Eur. J. Biochem. 222 (2), 313-323 (1994)	
MEDLINE	94291625	
PUBMED	8020470	
REFERENCE	2 (bases 1 to 1504)	
AUTHORS	Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E.	
TITLE	Molecular cloning of cDNA species for rat and mouse liver alpha-methylacyl-CoA racemases	
JOURNAL	Biochem. J. 326 (Pt 3), 883-889 (1997)	
MEDLINE	97439733	
PUBMED	9307041	
REFERENCE	3 (bases 1 to 1504)	
AUTHORS	Schmitz,W., Helander,H.M., Hiltunen,J.K. and Conzelmann,E.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-FEB-1997) Physiologic Chemistry II, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany	
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BASE COUNT	375 a 367 c 408 g 354 t	
ORIGIN		
Query Match	67.8%; Score 776.8; DB 10; Length 1504;	
Best Local Similarity	80.1%; Pred. No. 1.5e-165;	
Matches 913; Conservative	0; Mismatches 227; Indels 0; Gaps 0;	
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QY	67	GTCTGCGCTGACTTCGGGGCGCGGTGTGTACGCGGTGACCGGCCCCGCTCCCGCTACGAC 126
Db	62	ATCTGCGGGAAGCTTCGGCGCGAGGTGTGCTGCTGTGACAGACTGGGCTCCGTGAACCA 121
QY	127	GTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCAGCGCGGGGA 186
Db	122	CCAGTCACCTGGGCCGAGGCAAGCGCTCGCTGGCGCTGACCTGAAGCGGTCTCCGGGA 181
QY	187	GGCGCGCTGCTGCGGCGCTGTGCAAGCGGTCGGATGTGCTGTGAGACCCCTTCCGGCC 246
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QY	247	GGTGCATGGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGGAATAATCCAAGGCTT 306
Db	242	GGTGCATGGAGAACTCCAGCTTGGGCCAGAGACTCTACGGCAGGACAAATCCAAGCTC 301
QY	307	ATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGTGGCCAC 366
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QY	367	GATATCAACTATTGGCTTTGTGACGGTGTCTCTCAAAAAATTGGCAGAACTGGTGAGAAAT	426
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QY	487	GGCATTATATGGCTTTTGTGACCGCACACGCACTGGCAAGGCTCAGGTCATTGATGCA	546
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QY	547	AATATGGTGAAGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAATCAGAT	606
Db	542	AACATGGTGAAGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGGCGCATGGGT	601
QY	607	CTGTGGGAAGACCTCGAGAGACAGAACATGTTGATGTGTGAGACACCTTCTATACGACT	666
Db	602	CTGTGGGACACAGCTCGAGGAGCAAAACCTGTTAGATGGCGGGCACCCTTCTACACAACC	661
QY	667	TACAGGACAGCAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACCCAGTTCTACAGAG	726
Db	662	TACAGAGACCGCAGATGGGAGTTTCATGCGCTGTAGGTGCAATAGAACCCAGTTCTACACA	721
QY	727	CTGCTGATCAAAAGACCTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGATGAGATGGAT	786
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QY	787	GATTGGCCAGAAATGAAGAGAGTTTGCAGATGATTTTGCAAAAGAGACGAGAGCAGAG	846
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QY	847	TGTTGTCAAAATCTTTGACGGGACAGATGCCCTGTGTGACTCCGCTTCTGCACTTTGAGGAG	906
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QY	907	GTTCTTCATCATGATCACAACAAGAGAGGGGCTGCTTATCACCAGTGAGGAGCAGGAC	966
Db	902	GCCTTCACACACAGCACAACAAGAGAGGGGCTCCTTCATCATGATGAGGAGCAGCAT	961
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QY	1027	GATCCTTTTCATAGAGAGAACACACTGAGGAGATATCTGAAGAAATTTGATTACGCGCGAA	1086
Db	1022	GACCTTCTGTGGGAGAGACACTGTAGAGGTGCTTAAAGACTATGATTCAGTCAGGAA	1081
QY	1087	GAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAAGTAATAGGTAAGGCTAGTCTC	1146
Db	1082	GAGATTCATCAGCTGCACTGCACTGATGAATCATTTGAAGTAATATAGCTAAAGCCCACTC	1141
RESULT 12			
RN2ARYLCO			
LOCUS	RN2ARYLCO	1498 bp	linear
DEFINITION	R.noivegicus mRNA for 2-arylpropionyl-CoA epimerase.		
ACCESSION	Y08172		
VERSION	Y08172.1	GI:1552373	
KEYWORDS	2-arylpropionyl-CoA epimerase; epimerase.		
SOURCE	Rattus noivegicus.		
ORGANISM	Rattus noivegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 1498)		
AUTHORS	Reichel,C., Brugger,R., Bang,H., Geisslinger,G. and Brune,K.		
TITLE	Molecular cloning and expression of a 2-arylpropionyl-coenzyme A		
JOURNAL	epimerase: a key enzyme in the inversion metabolism of Ibuprofen		
MEDLINE	Mol. Pharmacol. 51 (4), 576-582 (1997)		
PUBMED	97260501		
	9106621		

REFERENCE	2 (bases 1 to 1498)
AUTHORS	Reichel, C.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-1996) C. Reichel, University Erlangen/Nuernberg, Dept. Exp./Clin. Pharmacology, Universitaetsstr. 22, D-91054 Erlangen, FRG
FEATURES	Location/Qualifiers
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ORIGIN	374 a 368 c 401 g 355 t
Query Match	65.8%; Score 753.8; DB 10; Length 1498;
Best Local Similarity	79.4%; Pred. No. 2,4e-160;
Matches 893; Conservative	0; Mismatches 232; Indels 0; Gaps 0;
QY	22 GTCGTGAGACTGTCCGCCCTGGCCCCGGCCGCTTCTGTCTATGCTCTGCTGACTTC 81
DB	7 GTACAGGTTCTGCGAGSCTTGCCCCAGGGCCGTTCTGCGGATGATCTCGCGACTTC 66
QY	82 GGGCGCGTGTGTACGCGTGGACCGCGCCCGCGCTCCCGCTACGACGTGAGCCGCTTGGCC 141
DB	67 GGGCGCGAGGTGTGTCTGTGACACACTGGCTCGGTGAACACCCAGTCACCTGCGCC 126
QY	142 CGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGGGAGCCCGCTGCTGCGG 201
DB	127 CGAGGCAAGCGCTCGCTGCGCTGACACTGAAGCGCTCTCCGGAGCCGCGGTGTGCGG 186
QY	202 CGTCTGTGCAAGCGGTGCGATGTGCTGCTTGAGCCCTTCCGCGCGCTCATGAGAAA 261
DB	187 CGCATGTCTTCACGCGCGGACGTGTGCTGAGCCCTCCGTTGCGGTATATGAGAAA 246
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DB	307 AGTGAATTTGGCCAGTCGCGGAATTTCTCCAAAGTACCTGGCCATGACATCAACTATGTG 366
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RESULT 13
BC015825 1472 bp mRNA linear ROD 07-AUG-2002
LOCUS BC015825
DEFINITION Mus musculus, alpha-methylacyl-CoA racemase, clone MGC:13903
IMAGE:3980103, mRNA, complete cds.
ACCESSION BC015825
VERSION BC015825.1 GI:16198362
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1472)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbioology.org>
contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 18 Row: C Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6678765.
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Best Local Similarity 79.6%; Pred. No. 1.9e-158;
Matches 894; Conservative 0; Mismatches 226; Indels 3; Gaps 1;
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QY 324 TGGATTTGGCCAGTCAAGAGCTTCTGCGCGTTAGCTGGCCACGATATCAACTATTTGGC 383
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QY 444 TCTCTGCTGCTACTTGTGCTGTGCTGCTTATGTGTGCTGCTGCTGCTGCTGCTGCT 503
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LOCUS	MMU89906	1515 bp	mRNA	linear	ROD 07-OCT-1997
DEFINITION	Mus musculus alpha-methylacyl-CoA racemase mRNA, complete cds.				
ACCESSION	U89906				
VERSION	U89906.1	GI:2145185			
KEYWORDS					
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1515)				
TITLE	Schmitz, W., Helander, H.M., Hiltunen, J.K. and Conzelmann, E.				
JOURNAL	Molecular cloning of cDNA species for rat and mouse liver alpha-methylacyl-CoA racemases				
MEDLINE	Biochem. J. 326 (Pt 3), 883-889 (1997)				
PUBMED	97439733				
REFERENCE	2 (bases 1 to 1515)				
AUTHORS	Schmitz, W., Helander, H.M., Hiltunen, J.K. and Conzelmann, E.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-FEB-1997) Physiologic Chemistry II, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany				
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Best Local Similarity	79.6%; Pred. No. 4e-156;				
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QY	699	TGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAAAGACTTTGACTTAAGCTGA	758
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Job time : 3422 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:42:24 ; Search time 1952.31 Seconds
(without alignments)
9506.702 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
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5: em_estov:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	850.4	74.2	955	12 BG741165	BG741165 602631843
3	812.8	70.9	842	9 AL551698	AL551698 AL551698
4	796.4	69.5	824	9 AL545355	AL545355 AL545355
5	795.2	69.4	873	9 AL555978	AL555978 AL555978
6	787.2	68.7	888	9 AL558977	AL558977 AL558977

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11	693	60.5	880	12	BG289921	BG289921 602381336
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13	652.8	57.0	812	12	BG035606	BG035606 602325670
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15	635.6	55.5	875	12	BE869129	BE869129 601445110
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19	605.8	52.9	713	10	AV714764	AV714764 AV714764
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25	546	47.6	914	12	BF796706	BF796706 602258327
26	545.6	47.6	672	14	BM714377	BM714377 UI-E-E30-
27	545.6	47.6	823	14	BM723657	BM723657 UI-E-E30-
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ALIGNMENTS

RESULT 1
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VERSION AL558928.1 GI:12903928
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
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Location/Qualifiers
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/db_xref="taxon:9606"
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/sex="male"
/tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 210 a 225 c 300 g 231 t 2 others
ORIGIN

Query Match 79.3%; Score 909.2; DB 9; Length 968;
Best Local Similarity 99.1%; Pred. No. 3e-245;
Matches 922; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

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Db 756 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGACTTCCCAATCAGATGAC 815
QY 781 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGACAGATGATTTGCAAAAGAGAGAG 840
Db 816 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGACAGATGATTTGCAAAAGAGAGAG-AR 874
QY 841 GCAGAGTGGTGTCAAAATCTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900

Db 875 GSAGAGTGTGTCAAAATCTTTGAGCGCACAGATGCGCTGTGACTCCGGTCTGACTTTT 934
QY 901 GAGAGGTTGTTTCATCATGATGACACAAG 930
Db 935 GAGAGGTTGTTTCATCATGATGACACAAG 964

RESULT 2
BG741165 955 bp mRNA linear EST 15-MAY-2001
LOCUS
DEFINITION
602631843F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',
mRNA sequence.
ACCESSION
BG741165
VERSION
BG741165.1 GI:14051818
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 955)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10630 row: f column: 12
High quality sequence stop: 805.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4776971"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 233 a 210 c 275 g 237 t
ORIGIN

Query Match 74.2%; Score 850.4; DB 12; Length 955;
Best Local Similarity 95.8%; Pred. No. 1.1e-228;
Matches 895; Conservative 0; Mismatches 36; Indels 3; Gaps 2;

QY 150 GCGCTCGCTAGTGTGACCTGAAGCAGCCGCGGGAGCGCGCTGCTGCGGCTGTGTG 209
Db 1 GCGCTCGCTAGTGTGACCTGAAGCAGCCGCGGGAGCGCGCTGCTGCGGCTGTGTG 60
QY 210 CAAGCGGTCGATGTGCTGTGAGACCCCTTCCGCGCGGTGCATGAGAACTCCAGCT 269
Db 61 CAAGCGGTCGATGTGCTGTGAGACCCCTTCCGCGCGGTGCATGAGAACTCCAGCT 120
QY 270 GGGCCACAGATTTCTGACGCGGGGAAATCCAGGCTTATTTATGCCAGGCTGATGAT 329
Db 121 GGGCCACAGATTTCTGACGCGGGGAAATCCAGGCTTATTTATGCCAGGCTGATGAT 180
QY 330 TGGCCAGTCAGGAAGCTTCTGCGCGGTAGCTGGCCACGATATCAACTATTGGCTTGTG 389
Db 181 TGGCCAGTCAGGAAGCTTCTGCGCGGTAGCTGGCCACGATATCAACTATTGGCTTGTG 240
QY 390 AGGTGTTCTCTCAAAAATGGCAGAGAGTGTGAGAAATCCGATGCCCCGCTGAATCTCCT 449
Db 241 AGGTGTTCTCTCAAAAATGGCAGAGAGTGTGAGAAATCCGATGCCCCGCTGAATCTCCT 300

QY 450 GGCTGACTTGTGCTGGGCTTATGTCACATGGCATTTAATGCTCTTTTGA 509
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 Db 301 GGCTGACTTGTGCTGGGCTTATGTCACATGGCATTTAATGCTCTTTTGA 360
 QY 510 CCGCACACGCTGCGCAGGCTCAGTCTATGATGCAATATGTTGGAAGAACAGCAT 569
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 Db 361 CCGCACACGCTGCGCAGGCTCAGTCTATGATGCAATATGTTGGAAGAACAGCAT 420
 QY 570 TTTAAGTCTTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAGACACTCGAGACA 629
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 Db 421 TTTAAGTCTTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAGACACTCGAGACA 480
 QY 630 GAACATGTTGATGGTGGAGCACCCTTCTATACGACTTACAGACAGCAGATGGGAAT 689
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 Db 481 GAACATGTTGATGGTGGAGCACCCTTCTATACGACTTACAGACAGATGGGAAT 540
 QY 690 CATGGCTGTGAGCAATAGAACCCCACTTCTACGAGCTGCTGATCAAGGACTTGGACT 749
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 Db 541 CATGGCTGTGAGCAATAGAACCCCACTTCTACGAGCTGCTGATCAAGGACTTGGACT 600
 QY 750 AAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATTTGGCCAGAAATGAAGAAG 809
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 Db 601 AAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATTTGGCCAGAAATGAAGAAG 660
 QY 810 GTTGCACATGTATTTGCAAGAAGACGAGAGAGTGTCAATCTTTGACGGCAC 869
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 Db 661 GTTGCACATGTATTTGCAAGAAGACGAGAGAGTGTCAATCTTTGACGGCAC 720
 QY 870 AGATGCTGTGTGACTCCGCTCTGACTTTTGGAGAGTGTTCATCATGATCACAACAA 929
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 Db 721 AGATGCTGTGTGACTCCGCTCTGACTTTTGGAGAGTGTTCATCATGATCACAACAA 780
 QY 930 GGAACGGGGCTCGTTTATCACCAGTGAAGAGCAGAGAC-GTGAGCCCCCGCTGCACCTC 988
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 Db 781 GGAACGGG--CTGTTATCACCAGTGAAGAGCAGAGAGTGCAGCCCCCGCTGCACCTC 838
 QY 989 TGCTGTTAAACACCCCACTCCCTCTTCAAAAGGATCCTTTCATAGAGAGAACACA 1048
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 Db 839 GGTGTTAAACACCCCACTCCCTCTTCAAAAGGATCCTTTCATAGAGAGAACACC 898
 QY 1049 CTGAGGAGATCTTGAAGAATTTGGATTCAGCCG 1082
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 Db 899 CTGAGGAGATCTTGAAGAATTTGGATTCAGCCG 932

RESULT 3
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 LOCUS AL551698 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI062YP05 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL551698
 VERSION AL551698.1 GI:12889898
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 842)
 L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /db_xref="taxon:9606"
 /clone="CSODI062YP05"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pcMVSPORT 6; site_1: NotI; 1st strand cDNA"

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 189 a 197 c 247 g 198 t 11 others
 ORIGIN

Query Match 70.9%; Score 812.8; DB 9; Length 842;
 Best Local Similarity 97.9%; Pred.No.4.4e-218;
 Matches 822; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

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 Db 4 ATGGCACTGCAAGGCGATCTCGGCTGTGAGCTGTCCGGCTGGCCCCCGGCGCTCTGT 63
 QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGGTGTGTACGCGTGGACCGCGCGCTCCGC 120
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 Db 64 GCTATGCTCTGGCTGACTTCGGGCGCGGTGTGTGTACGCGTGGACCGCGCGCTCCGC 123
 QY 121 TACGACGTAGCCGCTTGGCGCGGCGCAACCGCTCGCTAGTCTGTGACCTGGAAGCAGCCG 180
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 Db 124 TACGACSTAGCCGCTTGGCGCGGCGCAACCGCTCGCTAGTCTGTGACCTGGAAGCAGCCG 183
 QY 181 CGGGAGCGCCCGCTGCTGGCGCGCTGTGCAAGCGGTGGAATGTGCTGTGGAAGCCCTTC 240
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 Db 184 CGGGAGCGCCCGCTGCTGGCGCGCTGTGCAAGCGGTGGAATGTGCTGTGGAAGCCCTTC 243
 QY 241 CGCCGCGGTGTATGAGAACTCCAGCTGGGCGCCAGAGATTCGTGACGCGGGAATAATCA 300
 |||||||
 Db 244 CGCCGCGGTGTATGAGAACTCCAGCTGGGCGCCAGARATTTCTGACGCGGGAATAATCA 303
 QY 301 AGGCTTATTTATGCCAGGCTGAGTGTGGCCAGTCAAGAAAGCTTCTGCCGCTTAGCT 360
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 Db 304 AGGCTTATTTATGCCAGGCTGAGTGTGGCCAGTCAAGAAAGCTTCTGCCGCTTAGCT 363
 QY 361 GGGCAGATATCAACTATTTGGCTTTGTCAGGTGTTCTCAAAATTGGCAGAAAGTGT 420
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 Db 364 GGGCAGATATCAACTATTTGGCTTTKTGAGGTGTTCTCAAAATTGGCAGAAAGTGT 423
 QY 421 GAGAATCCGATGCCCCCGCTGAATCTCCGCTGACTTGTGCTGTGTGCTTATGTGT 480
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 Db 424 GAAATCCGATGCCCCCGCTGAATCTCCGCTGACTTGTGCTGTGTGCTTATGTGT 483
 QY 481 GCACTGGGCTTATTAATGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGTCAAT 540
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 Db 484 GCACTGGGCTTATTAATGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGTCAAT 543
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 QY 601 TCGAGTCTGTGGGAAGACACTCGAGACAAACATGTTGATGGTGGAGCACTTCTAT 660
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 Db 604 TCGAGTCTGTGGGAAGACACTCGAGACAAACATGTTGATGGTGGAGCACTTCTAT 663
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 Db 664 ACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGAGCAATAGAACCCAGTTC 723
 QY 721 TACGAGCTGCTGATCAAGAGACTTGGACTTAAGTCTGATGACTTCCCAATCAGATGAGC 780
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 Db 724 TACGAGCTGCTGATCAAGAGACTTGGACTTAAGTCTGATGACTTCCCAATCAGATGAGC 783
 QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTGTGAGATTAATTTGCAAGAAAGCAGAG 840
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 Db 784 ATGATGATTTGGCCAGAAATGAAGAAGTGTGAGATTAATTTGCAAGAAAGCAGAG 842

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RESULT 4
LOCUS      AL545355                      824 bp    mRNA    linear    EST 16-FEB-2001
DEFINITION AL545355 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI027YJ12 5
prime, mRNA sequence.
ACCESSION  AL545355
VERSION     AL545355.1  GI:12877836
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 824)
AUTHORS     Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/tissue_lib="LTI_NFL006_PL2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT  176 a 191 c 257 g 198 t 2 others
ORIGIN
Query Match 69.5%; Score 796.4; DB 9; Length 824;
Best Local Similarity 99.2%; Pred. No. 1.9e-213;
Matches 819; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

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Db 1 ACTGCAGGCATCTCGGTCGTGAGAGCTGCCGCGCCCGCGCTCTGTGCTAT 60

QY 66 GGTCTGGCTGACTTCGGGGCGCGTGTGCTAGCGGTGACCGCGCGCTCCGCTACGA 125
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Db 61 GGTCTGGCTGACTTCGGGGCGCGTGTGCTAGCGGTGACCGCGCGCTCCGCTACGA 120

QY 126 CGTAGCCGCTTGGGCGGGGCAAGCGCTGCTAGTGTGACTGAAGCAGCGCGGG 185
    |||||||
Db 121 CGTAGCCGCTTGGGCGGGGCAAGCGCTGCTAGTGTGACTGAAGCAGCGCGGG 180

QY 186 AGCCGCCCTGCTGCGGCGTGTGCAAGCGGTGATGTGCTGTGAGACCCCTTCGCGG 245
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Db 181 AGCCGCCCTGCTGCGGCGTGTGCAAGCGGTGATGTGCTGTGAGACCCCTTCGCGG 240

QY 246 CGGTGTGATGAGAACTCCAGCTGGGCGCCAGAGATTCTGACGCGGAAATCCAAAGGCT 305
    |||||||
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QY 306 TATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTTCGCGGTTAGCTGGCCA 365
    |||||||
Db 301 TATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTTCGCGGTTAGCTGGCCA 360

QY 366 CGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGCAGAACTGGTGAGAA 425
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Db 361 CGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGCAGAACTGGTGAGAA 420

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Db 421 TCCGTATGCCCGCGCTGAATCTCCGTGACTTTGCTGTGTGGCTTATGTGTCACT 480
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Db 660 TTACAGGACAGCAGATGGGGAATTTCATGCTGTTGGAGCAATAGAA-CCCAGTTCTACGA 718

QY 726 GCTGCTGATCAAGACCTTGACCTTAAGCTGTGATGACCTTCCCAATCAGATGAGCATGA 785
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Db 719 GCTGCTGATCAAGACCTTGACCTTAAGCTGTGATGACCTTCCCAATCAGATGAGCATGA 778

QY 786 TGATTTGGCCAGAAATGAGAGAAAGTTTCAGATGTATTTGCAAG 831
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Db 779 TGATTTGGCCAGAAATGAGAGAAAGTTTCAGATGTATTTTCAGAG 824

RESULT 5
LOCUS      AL555978                      873 bp    mRNA    linear    EST 16-FEB-2001
DEFINITION AL555978 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK010Y111 5
prime, mRNA sequence.
ACCESSION  AL555978
VERSION     AL555978.1  GI:12898227
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 873)
AUTHORS     Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/tissue_lib="LTI_NFL006_PL2"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT  180 a 208 c 278 g 204 t 3 others
ORIGIN
Query Match 69.4%; Score 795.2; DB 9; Length 873;
Best Local Similarity 99.4%; Pred. No. 4.1e-213;
Matches 805; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

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RESULT 6
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 DEFINITION AL558977 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ008YK07 5
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 ACCESSION AL558977
 VERSION AL558977
 KEYWORDS GI:12904022
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 888)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 180 a 213 c 281 g 209 t 5 others
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 Query Match 68.7%; Score 787.2; DB 9; Length 888;
 Best Local Similarity 99.1%; Pred. No. 7.5e-211;
 Matches 797; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
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 Db 85 ATGGCAGTGCAGGGCATCTGCGTCTGTGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGT 144
 QY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGGCTGAGCCGGCCGGCTCCGC 120
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 Db 625 GATGCAATATGTGTGAAGAAACAGCATATTTAAGTCTTTCTGTGTGAAAACCTCAGAAA 684
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 Db 685 TCGAGTCTGTGGGAAGCAGCTCGAGGACAGAAACATGTTGGATGTTGGAGCACTTTCTAT 744
 QY 661 ACGACTTACAGAGACAGCATGGGAATTCATGCGCTG-TTGAAGCAATAGAACCCAGTT 719

Db 745 ACGACTTACAGACAGACAGATGGGGAATTCATGCGTGTGGAGCAATARAACCCAGTT 804
QY 720 CTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGACTTCCCAATCAGATGAG 779
Db 805 CTACGARCTGCTGATCAAGGACTTGGACTAAAGTCTGATGACTTCCCAATCAGATGAG 864
QY 780 CATGGATGATGGCCAGAATGAA 803
Db 865 CATGGATGATGGCCARAATGAA 888
RESULT 7
AK002401
LOCUS 1523 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male kidney cDNA, RIKEN full-length enriched
library, clone:0610009H21:alpha-methylacyl-CoA racemase, full
insert sequence.
ACCESSION AK002401
VERSION AK002401.1 GI:12832356
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:0610009H21.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gliss,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
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Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamuya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzaelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Wittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S.

TITLE and Hayashizaki,Y.
JOURNAL Functional annotation of a full-length mouse cDNA collection
MEDLINE Nature 409 (6821), 685-690 (2001)
PUBMED 21085660
REFERENCE 11217851
AUTHORS 5 (bases 1 to 1523)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGCGGCCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0. Second strand cDNA
was prepared with the primer adapter of sequence[5'
GAGAGAGAGAGATCCACAGAGCCCAATTAATTAATTAACCCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.
FEATURES
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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BASE COUNT      365 a      386 c      414 g      358 t
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Query Match      66.4%; Score 760.4; DB 11; Length 1523;
Best Local Similarity 79.6%; Pred. No. 3.4e-203;
Matches 912; Conservative 0; Mismatches 231; Indels 3; Gaps 1;

QY 1 ATGGCACTGCAGGGCATCTCGGTGAGAGCTGTCCGGCCTGGCCCCGGCCGTTCTGT 60
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QY 61 GCTATGCTCTGCGCTGACTTCGGGGCGGTGTGTACCGCTGGACCGCGCCGCTCCCGC 120
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Db 83 GGAATGGTCTCTGGCGGACTTCGGCGCGGAGAGGTGTGCGCGCTGAACCGGCTGGGCTC--C 139

QY 121 TACGACGTGAGCCCGCTTGGCCCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
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Db 140 ACGGGCGAGAAATTTTCTGGCCCGAGGCAAGCGCTCGCTAGCGCTGAGCCTGAAGCGCTCT 199

QY 181 CGGGAGCCCGCGTGTCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 240
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QY 241 CGCCGCGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGGAATAATCCA 300
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Db 260 CGCTGCGGTGTATGAGAGAACTCCAGCTTGGGCCAGAGACTCTACTGCAAGACAAATCCA 319

QY 301 AGGCTATTATGCCAGGCTGAGTGTGAGTGTGGCCAGTCAGGAAGCTTTCGCGGTAGCT 360
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Db 320 AAGCTATCTATGCCAGGCTGAGCGGATTTGGCCAAATCGGGAATTTCTCCAAAGTAGCT 379

QY 361 GGCCAGATATACACTATTGGCTTTGCTTGCAGGTGTCTCTCAAAATTTGGCAGAGAGTGT 420
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Db 380 GGCCATGACATCAACTATTGGCTTTATCAGGCGTCTGTCAAAAGATTGGCAGAGCGGT 439

QY 421 GAGATCCGTTATGCCCGCTGAATTCCTGGCTGACTTGTGCTGTGCTGCTTATGCT 480
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Db 440 GAGAGCCCTTACCACCGCTGAATTCCTGGCTGACTTGTGGCGGTGAGGCCCTCATGTGC 499

QY 481 GCACCTGGCATTTATATGGCTCTTTTGAACCGCACAGCACTGGCAAGGGTCAAGTCAAT 540
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Db 500 ACACCTGGGCATTTGTCTGGCTCTCTTTGAACGACACAGCTCTGGCCGAGGGCAGGTCAATC 559

QY 541 GATGCAATATATGTGGAAGGAACAGCATTTTAAGTCTTTTCTGTGGAATAACTCAGAAA 600
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Db 560 GATTCAGCATGTGTGGAAGGAGCACTGCAATTAAGTCTTTCTGTGGAATAACTCAGAGCC 619

QY 601 TCGAGTCTGTGGGAGACACCTCGAGAGCAGAACATGTTGGATGTTGGAGCACCCTTTCTAT 660
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QY 661 ACGACTTACAGGACAGAGATGGGAATTCATGCTGTGGAGCAATAGAACCCAGTTTC 720
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Db 680 ACAACCTTACAAGAGCAGACGCGGAGTTTCAATGCTAGGTGCCATAGAACCCAGTTTC 739

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QY 841 GCAGAGTGTGTCAAAATCTTTGACGCGCAGAGATGCTGCTGTGACTCCGCTTCTGACTTTT 900
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Db 920 GAGAGGCTCTCCACACACAGCACAACAAGAACGGGCTCTTCATCATCTGATGGGAG 979

QY 961 CAGAGCGTACGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTC 1020
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Db 980 CAGCTCCGAGCCCCCGCTGCACCTCTGCTTTCAGAGACTCCTGCCGTCATCTGCC 1039

QY 1021 AAAAGGATCCTTTCATGAGAGACACACTGAGAGATCTGAAGAATTGGATTGAGC 1080
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Db 1100 CAGGAAGAGATCCTTACAGTGCACCTAGATAGAAATCGTTGAAAGTAAAGCTAAAGCC 1159

QY 1141 AGTCTC 1146
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Db 1160 AATCTC 1165

RESULT 8
BO962523
LOCUS
DEFINITION
BO962523 890 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8817570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6379327
5', mRNA sequence.
BO962523
BO962523.1 GI:22378001
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 890)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2566 row: c column: 08
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1. 890
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 187 a 221 c 278 g 203 t 1 others
ORIGIN

Query Match      64.6%; Score 739.8; DB 14; Length 890;
Best Local Similarity 99.1%; Pred. No. 1.8e-197;
Matches 744; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 9
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IMAGE:6203684 5', mRNA sequence.
ACCESSION BO941482
VERSION BO941482.1 GI:22356960
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM13623 row: 1 column: 21
High quality sequence stop: 621.
Location/Qualifiers

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source

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NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 253 a 189 c 219 g 223 t 6 others
ORIGIN

Query Match 63.5%; Score 728; DB 14; Length 890;
Best local Similarity 99.2%; Pred. No. 3.8e-194;
Matches 731; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 576 TTCTTTTCTGTGGAATACTCAGAAATGCACTGTGTGGAAGCACTCGAGACAGAAACAT 635
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Db 481 CTGTGTGACTCCGGTCTGACTTTTGAAGAGGTGTGTCATCATGATCACAACAAGAGAGC 540
QY 936 GGGCTCGTTTATCACCAGTGAG 995
Db 541 GGGCTCGTTTATCACCAGTGAG 600

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QY	1056	GATACCTTGAAGATTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACCTCAGATAAAAT	1115
Db	661	GATACCTTGAAGATTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACCTCAGATAAAAT	720
QY	1116	CATTGAAGTAATAAGG	1132
Db	721	CATTGAAGTAATAAGG	737
RESULT	10		
LOCUS	BI256255	808 bp	mRNA
DEFINITION	602975075F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114130 5',		
ACCESSION	BI256255		
VERSION	BI256255.1	GI:14810488	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 808)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LHAM11277 row: f column: 19 High quality sequence stop: 751.		
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source	location/Qualifiers		
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	/tissue_type="cervical carcinoma cell line"		
	/lab_host="DH10B"		
	/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."		
BASE COUNT	174 a	189 c	253 g
ORIGIN			192 t
Query Match	62.9%;	Score 720.6;	DB 13;
Best Local Similarity	98.1%;	Pred. No. 4.5e-192;	Length 808;
Matches 792;	Conservative	0;	Mismatches 9;
			Indels 6;
			Gaps 6;
QY	28	GAGCTGTCCGGCCCTGGCCCCGGCCCGCTTCTGTGCTATGCTGTGCTGACTTCGGGGCG	87
Db	1	GAGCTGTCCGGCCCTGGCCCCGGCCCGCTTCTGTGCTATGCTGTGCTGACTTCGGGGCG	60
QY	88	CGTGTGTACGCGCTGACCGCGCCCGGCTCCCGCTACGACGTGAGCGGCTTGGCGGGGGC	147
Db	61	CGTGTGTACGCGCTGACCGCGCCCGGCTCCCGCTACGACGTGAGCGGCTTGGCGGGGGC	120
QY	148	AAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCGCCGCGGGGAGCGCCGCTGTGCGGCGTCTG	207
Db	121	AAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCGCCGCGGGGAGCGCCGCTGTGCGGCGTCTG	180
QY	208	TGCAAGCGGTGGATGTGCTGTGTGAGCCCTTCGCGCGCGGTGTGTATGGAGAACTCCAG	267

Db	181	TCGCAAGCGGTCCGATGTGCTGCTGTGAGACCCCTTCCGCCGCCGGTGTTCATGGAGAAACTCCAG	240
QY	268	CTGGGCCCCAGAGATTCTGCAGCGCGGAAATCCAGGCTTATTATTCAGCGCTGAGTGA	327
Db	241	CTGGGCCCCAGAGATTCTGCAGCGCGGAAATCCAGGCTTATTATTCAGCGCTGAGTGA	300
QY	328	TTTGGCCAGTCAAGAAAGCTTCTCCCGTTAGCTGGCCACGATATCAACTATTGGCTTTG	387
Db	301	TTTGGCCAGTCAAGAAAGCTTCTCCCGTTAGCTGGCCACGATATCAACTATTGGCTTTG	360
QY	448	CTGGCTGACTTCTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTAATAGGCTTTT	507
Db	421	CTGGCTGACTTCTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTAATAGGCTTTT	480
QY	508	GACCGCACACGCACTGGCAAGGCTCAGGTCATTGATGCAATATGTGGAGAGACAGCA	567
Db	481	GACCGCACACGCACTGGCAAGGCTCAGGTCATTGATGCAATATGTGGAGAGACAGCA	540
QY	568	TATTTAAGTTCTTTCTGTGAAAACTCAGAAATCG-AGTCTGTGGAGACACCTGAGG	626
Db	541	TATTTAAGTTCTTTCTGTGAAAACTCAGAAATCG-AGTCTGTGGAGACACCTGAGG	600
QY	627	ACAGAACATGTGGATGGTGGAGACCTTCTATACGACTTACAGACAG-CAGATGGG	685
Db	601	ACAGAACATGTGGATGGTGGAGACCTTCTATACGACTTACAGACAG-CAGATGGG	660
QY	686	AATTCATGGCTGTTGGAGCAA-TAGAACCCCACTTCTACGAGCTGTCATCAAGACTT	744
Db	661	AATTCATGGCTGTTGGAGCAA-TAGAACCCCACTTCTACGAGCTGTCATCAAGACTT	720
QY	745	GGA-CTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAA	803
Db	721	GGA-CTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGATGATGATGGCCAGAAATGAA	779
QY	804	GAGCAAGTTTGCAGATGTATTGCCAA	830
Db	780	GAGCAAG-TTGCAGATGTATTGCCAA	805
RESULT 11			
LOCUS	880 bp	mrna	linear
DEFINITION	602381336F1 NIH_MGC_93	Homo sapiens	cdna clone IMAGE:4498977 5',
ACCESSION	CG289921		
VERSION	CG289921		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-r@mail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: L1AM10362 row: 9 column: 10		
	High quality sequence stop: 659.		
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source	1. 880		
	/organism="Homo sapiens"		

/db_xref="taxon:9606"
/clone="IMAGE:4498977"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT 180 a 235 c 270 g 195 t
ORIGIN

Query Match 60.5%; Score 693; DB 12; Length 880;
Best Local Similarity 97.4%; Pred. No. 2.8e-184;
Matches 737; Conservative 0; Mismatches 15; Indels 5; Gaps 3;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 60
Db 42 ATGGCACTGCAGGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 101
QY 61 GCTATGCTCTGGCTGACTTCGGGGCCGCTGTGTACGCGTGAGCCGGCCGCTCCCGC 120
Db 102 GCTATGCTCTGGCTGACTTCGGGGCCGCTGTGTGTACGCGTGAGCCGGCCGCTCCCGC 161
QY 121 TACGACGTGAGCCGCTTGGCCGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
Db 162 TACGACGTGAGCCGCTTGGCCGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 221
QY 181 CGGGAGCCCGCTGCTGCGCGCTGTGTCAAGCGGTGAGTGTGCTGTGAGCCCTTC 240
Db 222 CGGGAGCCCGCTGCTGCGCGCTGTGTCAAGCGGTGAGTGTGCTGTGAGCCCTTC 281
QY 241 CGCCGGGTGTCATGAGAACTCCAGCTGGGCCCAGAGATTCTGCACGGGAAATCCA 300
Db 282 CGCCGGGTGTCATGAGAACTCCAGCTGGGCCCAGAGATTCTGCACGGGAAATCCA 341
QY 301 AGGCTATTATTGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTCTGCCGGTTAGCT 360
Db 342 AGGCTATTATTGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTCTGCCGGTTAGCT 401
QY 361 GGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 420
Db 402 GGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 461
QY 421 GAGAAATCCGATATGCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGCTTATGTGT 480
Db 462 GAGAAATCCGATATGCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGCTTATGTGT 521
QY 481 GCACTGGGCATTATATGCTCTTTTGAACCCGACACGCACTGGCAAGGGTCAGTCAAT 540
Db 522 GCACTGGGCATTATATGCTCTTTTGAACCCGACACGCACTGGCAAGGGTCAGTCAAT 581
QY 541 GATGCAATATGTTGGAAGAACACATATTTAAGTCTTTCTGTGAAAAACTCAGAAA 600
Db 582 GATGCAATATGTTGGAAGAACACATATTTAAGTCTTTCTGTGAAAAACTCAGAAA 641
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGCTTGGTGGAGCACCTTTCTA 659
Db 642 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGCTTGGTGGAGCACCTTTCTA 701
QY 660 TACGACTTACAGGACAGCAGATGGG--AATTGATGGCTGTGGAG-CAATAGAACCC 715
Db 702 TACGACTTACAGGACAGCAGATGGGACATTCATGGCTGATGAGCCACTAGAACCC 761
QY 716 AGTTCTACGAGCTGCTGATCAAAAGACTTGACTAAA 752
Db 762 AAGTCTACGAGCTGCTGATCACAGACTTGGGCTAAA 798

RESULT 12
BG286300 935 bp mRNA linear EST 21-FEB-2001
LOCUS BG286300

DEFINITION 602382457F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4499990 5',
mRNA sequence.

ACCESSION BG286300
VERSION BG286300.1 GI:13039052
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 935)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10365 row: a column: 15
High quality sequence start: 4
High quality sequence stop: 701.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4499990"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT 190 a 246 c 299 g 200 t
ORIGIN

Query Match 57.9%; Score 664; DB 12; Length 935;
Best Local Similarity 96.1%; Pred. No. 4.4e-176;
Matches 713; Conservative 0; Mismatches 25; Indels 4; Gaps 3;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 60
Db 28 ATGGCACTGCAGGGCATCTCGTCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 87
QY 61 GCTATGCTCTGGCTGACTTCGGGGCCGCTGTGTACGCGTGAACCCGGCTCCCGC 120
Db 88 GCTATGCTCTGGCTGACTTCGGGGCCGCTGTGTGTACGCGTGAACCCGGCTCCCGC 147
QY 121 TACGACGTGAGCCGCTTGGCCGCGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG 180
Db 148 TACGACGTGAGCCGCTTGGCCGCGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG 207
QY 181 CGGGAGCCCGCTGCTGCGCGCTGTGTCAAGCGGTGAGTGTGCTGTGAGCCCTTC 240
Db 208 CGGGAGCCCGCTGCTGCGCGCTGTGTCAAGCGGTGAGTGTGCTGTGAGCCCTTC 267
QY 241 CGCCGGGTGTCATGAGAAATCCAGCTGGGCCCAGAGATTCTGCACGGGAAATCCA 300
Db 268 CGCCGGGTGTCATGAGAAATCCAGCTGGGCCCAGAGATTCTGCACGGGAAATCCA 327
QY 301 AGGCTATTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360
Db 328 AGGCTATTATGCGAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 387
QY 361 GGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 420
Db 388 GGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 447


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OY 421 GAGATCCGTATGCCCGCGCTGAATCTCTGGCTGACTTTGCTGTGTGGCCTTATGTGT 480
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Db 448 GAGATCCGTATGCCCGCGCTGAATCTCTGGCTGACTTTGCTGTGTGGCCTTATGTGT 507
OY 481 GCACTGGGCATTATATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAAT 540
      |||||||
Db 508 GCACTGGGCATTATATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGTCAAT 567
OY 541 GATGCAATATATGTGGAAGGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600
      |||||||
Db 568 TGATGCAATATGTGGAAGGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 627
OY 601 TCGAGTCTGTGGGAAGCACCCTCGAGGAC--AGACATGTTGGATGTGGAGCACCCTTCT 658
      |||||||
Db 628 TCGAGTCTGTGGGAAGCACCCTCGAGGACCAAGACCATGTGGATGTGGAGCACCCTTCT 687
OY 659 ATACGACTTACAGACA-GCAGATGGGAATTCATGGCTGTGTGAGCAATAGAACCCAG 717
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Db 688 ATACGACTTACAGACAAGCAGATGGCAATTCATGGCTG-TGAGCATTTGGAACCCAG 746
OY 718 TTCTACGAGCTGCTGATCAAG 739
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Db 747 TTCTACGAGCTGCGCATCAAG 768

RESULT 13
LOCUS BG035606 812 bp mRNA linear EST 24-JAN-2001
DEFINITION 602325670F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413833 5',
            mRNA sequence.
ACCESSION BG035606
VERSION BG035606.1 GI:12429907
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 812)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            JOURNAL Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10140 row: k column: 18
            High quality sequence stop: 672.
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                        /issue_type="adenocarcinoma, cell line"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 1.7 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC Library."
BASE COUNT 171 a 195 c 257 g 189 t

Query Match 57.0%; Score 652.8; DB 12; Length 812;
Best Local Similarity 99.6%; Pred. No. 6e-173;
Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 8 ATGGCACTGACAGGGCATCTCGGTATGAGAGCTGTCCGGCCTGGCCCCGGCCTTCTGT 67
OY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACCGCTGACCGCGCCGCTCCCGC 120
      |||||||
Db 68 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGTACCGCTGACCGCGCCGCTCCCGC 127
OY 121 TACGAGTGAAGCCGCTTGGCGCGGCAAGCGCTGCTAGTGTGACCTGAAGCAGCG 180
      |||||||
Db 128 TACGAGTGAAGCCGCTTGGCGCGGCAAGCGCTGCTAGTGTGACCTGAAGCAGCG 187
OY 181 CGGGAGCCCGCGCTGCTGCGCGCGTGTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 240
      |||||||
Db 188 CGGGAGCCCGCGCTGCTGCGCGCGTGTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 247
OY 241 CGCGCGGCTGTCAATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 300
      |||||||
Db 248 CGCGCGGCTGTCAATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 307
OY 301 AGCTTATTTATGCCAGCGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
      |||||||
Db 308 AGCTTATTTATGCCAGCGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 367
OY 361 GGCCAGCATATCAACTATTTGGCTTTGTGACCGCACAGCACTGGCAAGGTCAGTCAAT 420
      |||||||
Db 368 GGCCAGCATATCAACTATTTGGCTTTGTGACCGCACAGCACTGGCAAGGTCAGTCAAT 427
OY 421 GAGATCCGTATAGCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCCTTATGTGT 480
      |||||||
Db 428 GAGATCCGTATAGCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCCTTATGTGT 487
OY 481 GCACGTGGCATTTAATAGGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAGTCAAT 540
      |||||||
Db 488 GCACGTGGCATTTAATAGGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAGTCAAT 547
OY 541 GATGCAATATGTGGAAGGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600
      |||||||
Db 548 GATGCAATATGTGGAAGGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 607
OY 601 TCGAGTCTGTGGAAGCACCCTCGAGGACAGACATGTTGGATGTGTGAGCACCTTCTAT 660
      |||||||
Db 608 TCGAGTCTGTGGAAGCACCCTCGAGGACAGACATG-TGATGTGTGAGCACCTTCTAT 666
OY 661 ACGACTTA 668
      |||||||
Db 667 ACGACTTA 674

RESULT 14
LOCUS BQ638373 649 bp mRNA linear EST 15-JUL-2002
DEFINITION hd21909.Y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
ACCESSION BQ638373
VERSION BQ638373.1 GI:21762832
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 649)
            Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
            J.W., Bouffard,G., Smith,D. and Peterson,K.
            Expressed sequence tag analysis of human retina for the NEIBank
            Project: Retbindin, an abundant, novel retinal cDNA and alternative
            splicing of other retina-preferred gene transcripts
            Mol. Vis. 8 (4), (2002) In press
            Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078

JOURNAL
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Email: graeme@helix.nih.gov
 Plate: 21 row: g column: 09
 Seq primer: M13RP1 reverse primer (ABI).

FEATURES	Location/Qualifiers
source	1. .649

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/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-pGACTAGTTCAGATCGGAGCGGCCGCC(T)15-3'
]. EST analysis was performed on the unamplified library
at the NIH Intramural Sequencing Center (NISC)."
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Query Match	55.8%;	Score 640;	DB 14;	Length 649;
Best Local Similarity	99.2%;	Pred. No. 2.2e-169;		
Matches 643; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	142	CGGGGCAAGCGGCTCGCTAGTGTGCTGACCTGAAGCAGCCGGGGGAGCCGCCGCTGCGG	201
Db	2	CGCGTCCGGGCGCTCGCTAGTGTGCTGACCTGAAGCAGCCGGGGGAGCCGCCGCTGCGG	61
QY	202	CGTCTGTGCAAGCGGTCGGATGTGCTGTGAGCCCTTCGCCGCGGTGTGATGGAGAAA	261
Db	62	CGTCTGTGCAAGCGGTCGGATGTGCTGTGAGCCCTTCGCCGCGGTGTGATGGAGAAA	121
QY	262	CTCCAGCTGGGCCAGAGATTCTGACGGGGAAAATCCAAGGCTATTATGCCAGGCTG	321
Db	122	CTCCAGCTGGGCCAGAGATTCTGACGGGGAAAATCCAAGGCTATTATGCCAGGCTG	181
QY	322	AGTGCATTGGCCAGTCAGGAAGCTTTCGCCGTTAGCTGGCCACGATATCACTATTG	381
Db	182	AGTGCATTGGCCAGTCAGGAAGCTTTCGCCGTTAGCTGGCCACGATATCACTATTG	241
QY	382	GCCTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGTGAGAAATCCGTATGCCGCTG	441
Db	242	GCCTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAGTGTGAGAAATCCGTATGCCGCTG	301
QY	442	AAFTCTCTGGCTGACTTGTGCTGTGGTGGGCTTATGTGTGCACGTGGCATATTAATGGCT	501
Db	302	AAFTCTCTGGCTGACTTGTGCTGTGGTGGGCTTATGTGTGCACGTGGCATATTAATGGCT	361
QY	502	CTTTTTCACCCGACACGCACTGGCAAGGTCAGGTCATTGATGCCAATATGTTGCAAGGA	561
Db	362	CTTTTTCACCCGACACGCACTGGCAAGGTCAGGTCATTGATGCCAATATGTTGCAAGGA	421
QY	562	ACAGCATATTTAAGTCTTTTCTGTGAAAACCTCAGAAATCGAGTCTGTGGGAACCACT	621
Db	422	ACAGCATATTTAAGTCTTTTCTGTGAAAACCTCAGAAATCGAGTCTGTGGGAACCACT	481
QY	622	CGAGCAGAGAACATGTTGGATGTTGAGCACTTCTATACGACTTACAGACAGCAGAT	681
Db	482	CGAGCAGAGAACATGTTGGATGTTGAGCACTTCTATACGACTTACAGACAGCAGAT	541
QY	682	GGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTCTACGAGCTGCTGATCAAAGGA	741
Db	542	GGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTCTACGAGCTGCTGATCAAAGGA	601

QY 742 CTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGAT 789
|||||
Db 602 CTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGAT 649

RESULT 15					
BE869129					
LOCUS	BE869129	875 bp	mRNA	linear	EST 20-OCT-2000
DEFINITION	601445110F1 NIH_MGC_65	Homo sapiens	CDNA	clone IMAGE:3849147	5',
	mRNA sequence.				

ACCESSION	BE869129
VERSION	BE869129.1
KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
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/clone_1lb="NIH_MGC_65"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

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BASE COUNT	182	a	188	c	294	g	211	t
ORIGIN								
Query Match			55.5%;	Score 635.6;		DB 12;		Length 875;
Best Local Similarity			98.0%;	Pred. No. 4.4e-168;				
Matches 696;	Conservative		0;	Mismatches		9;	Indels	5;
							Gaps	5;

[illegible]

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Db 360 CAACATATTGGC-TTGTCAAGGTGTCTCFCAAAATTTGGCAGAGTGTGAGAAATCCGTA 418
QY 432 TGCCCCGCTGAATCTCCCTGGCTGACTTTGCTGTGGTGGCCCTTATGTGTGCACCTGGGCAT 491
Db 419 TGCCCCGCTGAATCTCCCTGGCTGACTTTGCTGTGGTGGCCCTTATGTGTGCACCTGGGCAT 478
QY 492 TATAATGGCTCTTTTGACCGCACAGCAGCTGGCAAGGTCAGGTCAATTGATGCAATAT 551
Db 479 TATAATGGCTCTTTTGACCG-ACACGCACTGACAAAGGTCAGGTCAATTGATGCAATAT 537
QY 552 GTGGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTG 611
Db 538 GTGGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTG 597
QY 612 GGAAGCACCTCGAGACAGAACATGTGGA-TGGTGGAGCACCTTTCTATACGACTTACA 670
Db 598 GGAAGCACCTCGAGACAGAACATGTGGAATGTGGAGACACCTTTCTATACGACTTACA 657
QY 671 GGACAGCAGAT-GGGGAATTTCATGGCTGTGGAGCAATAGAACCAGTT 719
Db 658 GGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCAGTTT 707

Search completed: April 2, 2003, 02:22:44
Job time : 1955.31 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 19:55:13 ; Search time 48.0076 Seconds
(without alignments)
7320.746 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcagggcatctc.....ataaggtaaaagctagtctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1142.8	99.7	1621	US-09-020-956-107	Sequence 107, App
2	1142.8	99.7	1621	US-09-030-607-107	Sequence 107, App
3	1142.8	99.7	1621	US-09-605-785-107	Sequence 107, App
4	1142.8	99.7	1621	US-09-439-313-107	Sequence 107, App
5	1142.8	99.7	1621	US-09-352-616A-107	Sequence 107, App
6	1142.8	99.7	1621	US-09-232-149A-107	Sequence 107, App
7	406.6	35.5	773	US-09-020-956-3	Sequence 3, Appl1
8	406.6	35.5	773	US-09-030-607-3	Sequence 3, Appl1
9	406.6	35.5	773	US-09-605-785-3	Sequence 3, Appl1
10	406.6	35.5	773	US-09-439-313-3	Sequence 3, Appl1
11	406.6	35.5	773	US-09-352-616A-3	Sequence 3, Appl1
12	406.6	35.5	773	US-09-232-149A-3	Sequence 3, Appl1
13	403.2	35.2	793	US-09-030-607-33	Sequence 33, Appl
14	403.2	35.2	793	US-09-605-785-33	Sequence 33, Appl
15	403.2	35.2	793	US-09-439-313-33	Sequence 33, Appl
16	403.2	35.2	793	US-09-352-616A-33	Sequence 33, Appl
17	403.2	35.2	793	US-09-232-149A-33	Sequence 33, Appl
18	403.2	35.2	793	US-09-020-956-2	Sequence 2, Appl1
19	400.2	34.9	816	US-09-030-607-2	Sequence 2, Appl1
20	400.2	34.9	816	US-09-605-785-2	Sequence 2, Appl1
21	400.2	34.9	816	US-09-439-313-2	Sequence 2, Appl1
22	400.2	34.9	816	US-09-352-616A-2	Sequence 2, Appl1
23	400.2	34.9	816	US-09-232-149A-2	Sequence 2, Appl1
24	316.4	27.6	421	US-09-222-575-116	Sequence 116, App
25	115	10.0	537	US-09-020-956-74	Sequence 74, Appl
26	115	10.0	537	US-09-030-607-74	Sequence 74, Appl
27	115	10.0	537	US-09-030-607-74	Sequence 74, Appl

28	115	10.0	537	4	US-09-605-785-74	Sequence 74, Appl
29	115	10.0	537	4	US-09-439-313-74	Sequence 74, Appl
30	115	10.0	537	4	US-09-352-616A-74	Sequence 74, Appl
31	115	10.0	537	4	US-09-232-149A-74	Sequence 74, Appl
32	66.2	5.8	328	4	US-09-605-785-672	Sequence 672, App
33	47	4.1	1412	1	US-08-097-831-1	Sequence 1, Appl1
34	46	4.0	1143	4	US-09-655-270A-4	Sequence 4, Appl1
35	46	4.0	1203	4	US-09-651-941-4	Sequence 4, Appl1
36	46	4.0	1203	4	US-09-955-597-4	Sequence 4, Appl1
37	46	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
38	46	4.0	12508	4	US-09-655-270A-1	Sequence 1, Appl1
39	46	4.0	12523	4	US-09-651-941-1	Sequence 1, Appl1
40	46	4.0	12523	4	US-09-955-597-1	Sequence 1, Appl1
41	44	3.8	2640	4	US-08-684-932A-37	Sequence 37, Appl
42	40.4	3.5	2214	3	US-08-864-038A-1	Sequence 1, Appl1
43	40.4	3.5	3331	3	US-08-864-038A-2	Sequence 2, Appl1
44	40.4	3.5	3331	3	US-08-864-038A-4	Sequence 4, Appl1
45	40	3.5	529	4	US-09-159-106-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-020-956-107
; Sequence 107, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCACCTGCAGGCGATCTCGGTCTGAGAGCTGTCGCGCCCTGGCCCGGCGCCGCTTCTGT 60
Db 5 ATGCACCTGCAGGCGATCTCGGTCTGAGAGCTGTCGCGCCCTGGCCCGGCGCCGCTTCTGT 64

QY 61 GCTATGCTCCTGCTGACTTTCGGGGCGCGTGTGCTACCGCTGGACCGCGCCGCTCCCGC 120
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Db 65 GCTATGCTCCTGCTGACTTTCGGGGCGCGTGTGCTACCGCTGGACCGCGCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
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Db 125 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 184
QY 181 CGGGGAGCCCGCTGCTGCGGGCGTCTGTGCAAGCGCTCGGATGTGCTGCTGAGCCCTTC 240
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Db 185 CGGGGAGCCCGCTGCTGCGGGCGTCTGTGCAAGCGCTCGGATGTGCTGCTGAGCCCTTC 244
QY 241 CGCCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
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Db 245 CGCCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 304
QY 301 AGGCTTATTTATGCGCAGCGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
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Db 305 AGGCTTATTTATGCGCAGCGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
QY 361 GGGCAGCATATCACTATTGGCTTTGTGAGGTCTCTCAAAAATTTGGCAGAGTGTG 420
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Db 365 GGGCAGCATATCACTATTGGCTTTGTGAGGTCTCTCAAAAATTTGGCAGAGTGTG 424
QY 421 GAGAATCCGTATGCCCCGCTGATCTCCTGGCTGACTTTGCTGTGTGGCTTATGTGT 480
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Db 425 GAGAATCCGTATGCCCCGCTGATCTCCTGGCTGACTTTGCTGTGTGGCTTATGTGT 484
QY 481 GCACCTGGCATTTAATGCTCTTTTGACCCGACACGCACTGGCAAGGCTCAGTCAAT 540
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Db 485 GCACCTGGCATTTAATGCTCTTTTGACCCGACACGCACTGGCAAGGCTCAGTCAAT 544
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Db 545 GATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGGAATACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAACTGTGGATGTGGAGCACCTTCTAT 660
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Db 605 TCGAGTCTGTGGGAAGCACTCGAGGACAGAACTGTGGATGTGGAGCACCTTCTAT 664
QY 661 ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 720
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Db 665 ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 724
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
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Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY 781 ATGGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTGGCAAGAAGACGAAG 840
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Db 785 ATGGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTGGCAAGAAGACGAAG 844
QY 841 GCAGAGTGTCTCAAACTTTTGACGGCACAGATGCCGTGTGACTCCGGTTCTGACTTTT 900
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Db 845 GCAGAGTGTCTCAAACTTTTGACGGCACAGATGCCGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGTGTTCATCATGATCACACAAGGAACGGGCTGTTTATCACCAGTGAAGAG 960
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Db 905 GAGGAGTGTTCATCATGATCACACAAGGAACGGGCTGTTTATCACCAGTGAAGAGAG 964
QY 961 CAGGACGTGAGCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTC 1020
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Db 965 CAGGACGTGAGCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTC 1024
QY 1021 AAAAGGATCCTTTCAATAGGAGAACAACACTGAGAGATTAATTGAAGAATTTGATTCAGC 1080
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Db 1025 AAAAGGATCCTTTCAATAGGAGAACAACACTGAGAGATTAATTGAAGAATTTGATTCAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAAGTCAATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1140
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Db 1085 CGCGAAGAGATTTATCAGCTTAAGTCAATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1144

QY 1141 AGTCTC 1146
|||||
Db 1145 AGTCTC 1150
RESULT 2
US-09-030-607-107
; Sequence 107, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206).622-4900
; TELEFAX: (206).682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-107
Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCACTGACGGGCACTCGGTGCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 60
|||||
Db 5 ATGCACTGACGGGCACTCGGTGCTGAGCTGTCGGCCCTGGCCCCGGCCGTTCTGT 64
QY 61 GCTATGCTCCTGCTGACTTTCGGGGCGCGTGTGCTACCGCTGGACCGCGCCGCTCCCGC 120
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Db 65 GCTATGCTCCTGCTGACTTTCGGGGCGCGTGTGCTACCGCTGGACCGCGCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
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Db 125 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 184
QY 181 CGGGGAGCCCGCTGCTGCGGGCGTCTGTGCAAGCGCTCGGATGTGCTGCTGAGCCCTTC 240
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Db 185 CGGGGAGCCCGCTGCTGCGGGCGTCTGTGCAAGCGCTCGGATGTGCTGCTGAGCCCTTC 244
QY 241 CGCCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
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Db 245 CGCCGCGGTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 304
QY 301 AGGCTTATTTATGCGCAGCGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360

Db	305	AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTACAGGAAGCTTCTGCGGTTAGCT	364
QY	361	GGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGGCAGAAAGTGGT	420
Db	365	GGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGGCAGAAAGTGGT	424
QY	421	GAGATCCGTATGCCCCGCTGAATCTCTGCGTGACTTTGCTGTGTGGTGGCCTTATGTGT	480
Db	425	GAGAAATCCGTATGCCCCGCTGAATCTCTGCGTGACTTTGCTGTGTGGTGGCCTTATGTGT	484
QY	481	GCACCTGGCATTTAATATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGTCAGTCAATT	540
Db	485	GCACCTGGCATTTAATATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGTCAGTCAATT	544
QY	541	GATGCAAAATATGCTGGAAGGAAACAGCATATTTAAGTCTTTCTGTGTGAAAACTCAGAAA	600
Db	545	GATGCAAAATATGCTGGAAGGAAACAGCATATTTAAGTCTTTCTGTGTGAAAACTCAGAAA	604
QY	601	TGCAGTCTGTGGGAAGCACCTCGAGAGCAGACATGTTGATGGTGGAGCACCTTTCTAT	660
Db	605	TGCAGTCTGTGGGAAGCACCTCGAGAGCAGACATGTTGATGGTGGAGCACCTTTCTAT	664
QY	661	ACGACTTTACAGACAGCAGATGGGGAAATTCATGGCTGTTGAGCAATAGAAACCCAGTTTC	720
Db	665	ACGACTTTACAGACAGCAGATGGGGAAATTCATGGCTGTTGAGCAATAGAAACCCAGTTTC	724
QY	721	TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCATCAGATGAGC	780
Db	725	TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCATCAGATGAGC	784
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTGCAAAAGAGAAGCAAG	840
Db	785	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTGCAAAAGAGAAGCAAG	844
QY	841	GCAGAGTGTGTCCAAATCTTTGACGGGCACAGATGCGCTGTGTGACTCCGGTTCGACTTTT	900
Db	845	GCAGAGTGTGTCCAAATCTTTGACGGGCACAGATGCGCTGTGTGACTCCGGTTCGACTTTT	904
QY	901	GAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGAG	960
Db	905	GAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGAG	964
QY	961	CAGGACGTGAGCCCCGCGCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1020
Db	965	CAGGACGTGAGCCCCGCGCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1024
QY	1021	AAAAGGATCCTTTTCATAGAGAAACACACTGAGAGATACTTGAAGAATTGGATTGCAGC	1080
Db	1025	AAAAGGATCCTTTTCATAGAGAAACACACTGAGAGATACTTGAAGAATTGGATTGCAGC	1084
QY	1081	CGCGAAGAGATTTATCAGCTTAACCTCAGATTAATAATCATTTGAAAGTAAATAAGCT	1140
Db	1085	CGCGAAGAGATTTATCAGCTTAACCTCAGATTAATAATCATTTGAAAGTAAATAAGCT	1144
QY	1141	AGTCTC 1146	
Db	1145	AGTCTC 1150	

RESULT 3
US-09-605-785-107
; Sequence 107, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaogchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Heppler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-107

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Query Match	99.7%;	Score 1142.8;	DB 4;	Length 1621;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1144;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;
QY 1	ATGGCACTGCAGAGGCAATCTCGGTCTGCGAGCTGTCCGCGCTGGCCCGCCCGCTTCTGT	60		
Db 5	ATGGCACTGCAGAGGCAATCTCGGTCTGCGAGCTGTCCGCGCTGGCCCGCCCGCTTCTGT	64		
QY 61	GCTATGCTCTTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC	120		
Db 65	GCTATGCTCTTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC	124		
QY 121	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCGG	180		
Db 125	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCGG	184		
QY 181	CGGGGAGCCCGCGTGTCTGGGCGGTCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC	240		
Db 185	CGGGGAGCCCGCGTGTCTGGGCGGTCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC	244		
QY 241	CGCCGGGGTGTCACTGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCA	300		
Db 245	CGCCGGGGTGTCACTGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCA	304		
QY 301	AGGCTTATTTATGCCAAGCTGAGTGGATTTGGCCAGTCAAGGAAGCTTCTGCCGTTAGCT	360		
Db 305	AGGCTTATTTATGCCAAGCTGAGTGGATTTGGCCAGTCAAGGAAGCTTCTGCCGTTAGCT	364		
QY 361	GGCCACGATATCAACTATTTGGCTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAACTGCT	420		
Db 365	GGCCACGATATCAACTATTTGGCTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAACTGCT	424		
QY 421	GAGATCCGATATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGTGTGGCTTATGTGT	480		
Db 425	GAGATCCGATATGCCCCGCTGAATCTCTGCTGCTGACTTTGCTGTGTGGCTTATGTGT	484		
QY 481	GCACGTGGGCAATTATTAATGGCTCTTTTGAACCGACACGCACTGGCAAGGTCAGTCAATT	540		
Db 485	GCACGTGGGCAATTATTAATGGCTCTTTTGAACCGACACGCACTGGCAAGGTCAGTCAATT	544		
QY 541	GATGCAATATATGTTGGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA	600		
Db 545	GATGCAATATATGTTGGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA	604		
QY 601	TGCACTCTGTGGGAGCACCTCGAGAGCAGAACATGTTGGATGTGTGAGCACCTTCTAT	660		
Db 605	TGCACTCTGTGGGAGCACCTCGAGAGCAGAACATGTTGGATGTGTGAGCACCTTCTAT	664		
QY 661	ACGACTTACAGAGACAGATGGGCAATTCAATGGCTCTGTGGAGCAATAGAACCCCACTTC	720		
Db 665	ACGACTTACAGAGACAGATGGGCAATTCAATGGCTCTGTGGAGCAATAGAACCCCACTTC	724		

QY 721 TACGAGCTGCTGATCAAAAGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTCAGATGTATTGGCAAGAAGACGAAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAGAGTTCAGATGTATTGGCAAGAAGACGAAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT 904
QY 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAGTAGAGAG 960
Db 905 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAGTAGAGAG 964
QY 961 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTC 1020
Db 965 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATGATGAAGATTTGGATTGAGC 1080
Db 1025 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATGATGAAGATTTGGATTGAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATGGAAGTAATGAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATGGAAGTAATGAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 4
US-09-439-313-107
; Sequence 107, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439, 313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCGACTGCAGGCACTCGGTGCTGAGAGTGTCCGGCTGGCCCCGGCCGTTCTGT 60
Db 5 ATGCGACTGCAGGCACTCGGTGCTGAGAGTGTCCGGCTGGCCCCGGCCGTTCTGT 64
QY 61 GCTATGCTCTGCTGACTTCGGGGCGGCTGTGTACGCGTGAACCGGGCCGCTCCCGC 120
Db 1145 AGTCTC 1150

Db 65 GCTATGCTCTGCTGACTTCGGGGCGGCTGTGTGTACGCGTGAACCGGGCCGCTCCCGC 124
QY 121 TACGAGGTGAGCCGCTTGGGGCGGGAAGCCGCTGCTAGTCTGGACCTGAAGCAGCCG 180
Db 125 TACGAGGTGAGCCGCTTGGGGCGGGAAGCCGCTGCTAGTCTGGACCTGAAGCAGCCG 184
QY 181 CGGGGAGCCCGGCTGCTGCGGCTGTGCAAGCGGTGAGTGTGCTGTGAGCCCTTC 240
Db 185 CGGGGAGCCCGGCTGCTGCGGCTGTGCAAGCGGTGAGTGTGCTGTGAGCCCTTC 244
QY 241 CGCCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATCTGCAGCGGAAATCCA 300
Db 245 CGCCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATCTGCAGCGGAAATCCA 304
QY 301 AGGCTATTATGCCAGCGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTATTATGCCAGCGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 364
QY 361 GGGCAGCATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAAGTGT 420
Db 365 GGGCAGCATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAAGTGT 424
QY 421 GAGATCCGTATGCCCCGCTGAATCTCTGCTGACTTGTCTGTGCTGCTGCTTATGTGT 480
Db 425 GAGATCCGTATGCCCCGCTGAATCTCTGCTGACTTGTCTGTGCTGCTGCTTATGTGT 484
QY 481 GCATGCGCATTTATATGCTCTTTTGAACCGCACACGCACTGCAAGGGTCAAGTCAATT 540
Db 485 GCATGCGCATTTATATGCTCTTTTGAACCGCACACGCACTGCAAGGGTCAAGTCAATT 544
QY 541 GATGCAATATGTTGGAAGGAACACATATTTAAGTCTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAATATGTTGGAAGGAACACATATTTAAGTCTTTCTGTGAAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGACAGACATGTTGATGCTGAGCACCTTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGACAGACATGTTGATGCTGAGCACCTTTCTAT 664
QY 661 ACGACTTACAGAGACAGACAGATGGGAATTTCATGCTGTTGGACCAATAGAACCCAGTTTC 720
Db 665 ACGACTTACAGAGACAGACAGATGGGAATTTCATGCTGTTGGACCAATAGAACCCAGTTTC 724
QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGAGATGTATTGGCAAGAAGACGAAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGAGATGTATTGGCAAGAAGACGAAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT 904
QY 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAGTAGAGAG 960
Db 905 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAGTAGAGAG 964
QY 961 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTC 1020
Db 965 CAGGAGGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATGATGAAGATTTGGATTGAGC 1080
Db 1025 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATGATGAAGATTTGGATTGAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATGGAAGTAATGAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATGGAAGTAATGAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150


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RESULT 5
US-09-352-616A-107
; Sequence 107, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-107
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Query Match          99.78; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.88; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGT 64
QY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGGCCGCTCCCGC 120
Db 65 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGTACGCGTGGACCGGGCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGCGCCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGCGCCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCCG 184
QY 181 CGGGAGCCCGCGTGTGCGCGCTGTGTGCAAGCGGTCCGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGAGCCCGCGTGTGCGCGCTGTGTGCAAGCGGTCCGATGTGCTGTGAGCCCTTC 244
QY 241 CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCCAAGAGATTCTGCAGCGGGAATCCA 300
Db 245 CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCCAAGAGATTCTGCAGCGGGAATCCA 304
QY 301 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGGTTAGCT 360
Db 305 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGGTTAGCT 364
QY 361 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTTGGCAGAAGTGT 420
Db 365 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTTGGCAGAAGTGT 424
QY 421 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTCGTGGTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTCGTGGTGGTGGCTTATGTGT 484
QY 481 GCACTGGGATTTATATGCTCTTTTGGACCGCACAGCAGCTGGCAAGGTCAGGTCAAT 540
Db 485 GCACTGGGATTTATATGCTCTTTTGGACCGCACAGCAGCTGGCAAGGTCAGGTCAAT 544
QY 541 GATGCAAAATATGTTGGAAGAACAGCATATTAAATCTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGTTGGAAGAACAGCATATTAAATCTTTCTGTGAAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCAGCTCGAGGACAGACATGTTGATGCTGGAGCACTTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCAGCTCGAGGACAGACATGTTGATGCTGGAGCACTTTCTAT 664
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QY 661 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGCAGATGTATTGCAAGAGAGAG 840
Db 785 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGCAGATGTATTGCAAGAGAGAG 844
QY 841 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTTGACTTTT 900
Db 845 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTTGACTTTT 904
QY 901 GAGGAGTTGTTTCATCATGATCACAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCACAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 964
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCTTTTCATAGAGAAACACACTGAGAGATACTGAAGAATTTGATTCAGC 1080
Db 1025 AAAAGGATCTTTTCATAGAGAAACACACTGAGAGATACTGAAGAATTTGATTCAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACACTCAGATTAATCATTTGAAAGTAAATGAGT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACACTCAGATTAATCATTTGAAAGTAAATGAGT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150
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RESULT 6
US-09-232-149A-107
; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-107
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Query Match          99.78; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.88; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGT 64
QY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGGCCGCTCCCGC 120
Db 65 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTGTACGCGTGGACCGGGCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGCGCCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGCGCCGGGGCAAGCGCTCGTAGTCTGAGCTGAAGCAGCCG 184
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QY 181 CGGGGAGCCCGCTGCTGCGGGGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGGAGCCCGCTGCTGCGGGGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 244
QY 241 CGCCGCGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAGAAATCCA 300
Db 245 CGCCGCGGTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAGAAATCCA 304
QY 301 AGGCTTATTATGCGCAGCTGAGTGAGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTTATTATGCCAGGCTGAGTGAGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 364
QY 361 GGGCAGCATATCAACTATTGGCTTTGTACAGGTGTCTCTCAAAATTTGGCAGAGTGT 420
Db 365 GGGCAGCATATCAACTATTGGCTTTGTACAGGTGTCTCTCAAAATTTGGCAGAGTGT 424
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGGTGGCTTATGTGT 480
Db 425 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGGTGGCTTATGTGT 484
QY 481 GCACTGGCATATATATGGCTCTTTTGACCCGACAGCATGGCAAGGTCAGTCAAT 540
Db 485 GCACTGGCATATATATGGCTCTTTTGACCCGACAGCATGGCAAGGTCAGTCAAT 544
QY 541 GATGCAATATATGTGAGAGAAACAGCATATTAAAGTCTTTCTGTGMAAACTCAGAAA 600
Db 545 GATGCAATATATGTGAGAGAAACAGCATATTAAAGTCTTTCTGTGMAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGAGACACCTCGAGGACAGAACTGTGATGTGTGAGCACCCTTCTAT 660
Db 605 TCGAGTCTGTGGAGACACCTCGAGGACAGAACTGTGATGTGTGAGCACCCTTCTAT 664
QY 661 ACGACTTACAGACAGAGATGGGAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGACAGAGATGGGAATTCATGGCTTTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTTCATGAATTCATCCATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTTCATGAATTCATCCATCAGATGAGC 784
QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTGGCAGATGTATTGGCAAGAAGACGAG 840
Db 785 ATGATGATTGGCCAGAAATGAAGAAGATTGGCAGATGTATTGGCAAGAAGACGAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGTGTGTCAATCATGATCAACAAGGAAGGCTCGTTTATCACCAGTGAAGAG 960
Db 905 GAGGAGTGTGTCAATCATGATCAACAAGGAAGGCTCGTTTATCACCAGTGAAGAG 964
QY 961 CAGGAGCTGAGCCCGCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGGAGCTGAGCCCGCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGATTCAGC 1080
Db 1025 AAAAGGATCTTTTATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGATTCAGC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAATCAGATTAATATGAAAGTAATAGGTAAGAAAGCT 1140
Db 1085 CGCGAAGAGATTATCAGCTTAATCAGATTAATATGAAAGTAATAGGTAAGAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 7
US-09-020-956-3/c
; Sequence 3, Application US/09020956

; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mak1, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-020-956-3

Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. NO. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GCGAAGCACCCTGAGAGACAGAACTGTGTGATGGTGGAGCACCTTCTATACGACTTACA 670
Db 415 GGGCCCCCCTCGAGAGACAGAACTGTGTGATGGTGGAGCACCTTCTATACGACTTACA 356
QY 671 GCACAGCAGATGGGAATTCATGGCTGTGTGAGCAATAGAACCCAGTCTACAGCTGC 730
Db 355 GCACAGCAGATGGGAATTCATGGCTGTGTGAGCAATAGAACCCAGTCTACAGCTGC 296
QY 731 TGATCAAGGACTTGGACTTAAAGTCTGATGAATTCATCAATCAGATGAGCATGATGATT 790
Db 295 TGATCAAGGANNNTGACTTAAAGTCTGATGAATTCATCAATCAGATGAGCATGATGATT 236
QY 791 GGGCAGAAATGAAGAAGATTGGCAGATGTATTGCAAGAAGAGAGAGAGAGAGTGT 850
Db 235 GGGCAGAAATGAAGAAGATTGGCAGATGTATTGCAAGAAGAGAGAGAGAGAGTGT 176
QY 851 GTCAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAAGAGTGT 910
Db 175 GTCAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAAGAGTGT 116
QY 911 TTCATCATGATCACACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 970
Db 115 TTCATCATGATCACACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 56
QY 971 GCGCCCGCCCTGACCTGTCTGTAAACACCCAGCCATCCCTTCTTCAAAAG 1025
Db 55 GCGCCCGCCCTGACCTGTCTGTAAACACCCAGCCATCCCTTCTTCAAAAG 1

RESULT 8
US-09-030-607-3/c

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; Sequence 3, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-030-607-3
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Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGAAGACCTCGAGGACAGACATGTTGGATGGTGAGCACCCTTTCTATACGACTTACA 670
DB 415 GGGCCCCCTCGAGGACAGACATGTTGGATGGTGAGCACCCTTTCTATACGACTTACA 356
QY 671 GGACAGCAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 730
DB 355 GGACAGCAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 296
QY 731 TGATCAAGGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATT 790
DB 295 TGATCAAGGANNTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATT 236
QY 791 GGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAGAAGAGCAAGGAGAGTGGT 850
DB 235 GGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAGAAGAGCAAGGAGAGTGGT 176
QY 851 GTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGGTTG 910
DB 175 GTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGGTTG 116
QY 911 TTCATCATGATCACACAAGAGAGCGGGCTCGTTATACCAAGTGAAGAGAGAGAGCTGA 970
DB 115 TTCATCATGATCACACAAGAGAGCGGGCTCGTTATACCAAGTGAAGAGAGAGAGCTGA 56
QY 971 GCGCCCGCCCTGACACTCTGCTGTTAAACACCCAGCCATCCCTTTTCAAAAG 1025
DB 55 GCGCCCGCCCTGACACTCTGCTGTTAAACACCCAGCCATCCCTTTTCAAAAG 1
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RESULT 9

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US-09-605-785-3/c
; Sequence 3, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harlocker, Susan L.
; STREET: Harlocker, Susan L.
; CITY: Harlocker, Susan L.
; STATE: Harlocker, Susan L.
; COUNTRY: Harlocker, Susan L.
; ZIP: Harlocker, Susan L.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Harlocker, Susan L.
; COMPUTER: Harlocker, Susan L.
; OPERATING SYSTEM: Harlocker, Susan L.
; SOFTWARE: Harlocker, Susan L.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/605,785
; FILING DATE: 2000-06-27
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Harlocker, Susan L.
; REGISTRATION NUMBER: 210121.427C16
; REFERENCE/DOCKET NUMBER: 2000-06-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: Harlocker, Susan L.
; TELEFAX: Harlocker, Susan L.
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc_feature
; LOCATION: (1)..(773)
; OTHER INFORMATION: n = A,T,C or G
; US-09-605-785-3
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Query Match 35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGAAGACCTCGAGGACAGACATGTTGGATGGTGAGCACCCTTTCTATACGACTTACA 670
DB 415 GGGCCCCCTCGAGGACAGACATGTTGGATGGTGAGCACCCTTTCTATACGACTTACA 356
QY 671 GGACAGCAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 730
DB 355 GGACAGCAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGC 296
QY 731 TGATCAAGGACTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATT 790
DB 295 TGATCAAGGANNTTGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATT 236
QY 791 GGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAGAAGAGCAAGGAGAGTGGT 850
DB 235 GGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAGAAGAGCAAGGAGAGTGGT 176
QY 851 GTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGGTTG 910
DB 175 GTCAAAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGGTTG 116
QY 911 TTCATCATGATCACACAAGAGAGCGGGCTCGTTATACCAAGTGAAGAGAGAGAGCTGA 970
DB 115 TTCATCATGATCACACAAGAGAGCGGGCTCGTTATACCAAGTGAAGAGAGAGAGCTGA 56
QY 971 GCGCCCGCCCTGACACTCTGCTGTTAAACACCCAGCCATCCCTTTTCAAAAG 1025
DB 55 GCGCCCGCCCTGACACTCTGCTGTTAAACACCCAGCCATCCCTTTTCAAAAG 1
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RESULT 10
US-09-439-313-3/c

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; Sequence 3, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-3
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Query Match          35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGAAGCACCCTCGAGCAGAACATGTTGGATGGTGAGCACCTTCTATACGACTTACA 670
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 415 GGGCCCCCCTCGAGCAGAACATGTTGGATGGTGAGCACCTTCTATACGACTTACA 356

QY 671 GGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 730
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 355 GGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 296

QY 731 TGATCAAGGACTTGACTTAAGTCTGATGACTTCCCAATCAGATGAGCATGATGATT 790
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 TGATCAAGGANNTTGACTTAAGTCTGATGACTTCCCAATCAGATGAGCATGATGATT 236

QY 791 GGGCAGAAATGAGAAGAACTTTGCAGATGATTTGCAAGAAGACGAAGGCAGAGTGT 850
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 GGGCAGAAATGAGAAGAACTTTGCAGATGATTTGCAAGAAGACGAAGGCAGAGTGT 176

QY 851 GTCAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGAGGTTG 910
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 GTCAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGAGGTTG 116

QY 911 TTCATCATGATCACAACAAGAAAGCGGGCTCGTTTATCACCAGTGAGAGCAGAGCTGA 970
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 TTCATCATGATCACAACAAGAAAGCGGGCTCGTTTATCACCAGTGAGAGCAGAGCTGA 56

QY 971 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1025
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Db 55 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1
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RESULT 11
US-09-352-616A-3/C
; Sequence 3, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqul
; APPLICANT: Xu, Jiangchun
```

```
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-3
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Query Match          35.5%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 6e-107;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 611 GGAAGCACCCTCGAGCAGAACATGTTGGATGGTGAGCACCTTCTATACGACTTACA 670
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QY 791 GGGCAGAAATGAGAAGAACTTTGCAGATGATTTGCAAGAAGACGAAGGCAGAGTGT 850
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Db 235 GGGCAGAAATGAGAAGAACTTTGCAGATGATTTGCAAGAAGACGAAGGCAGAGTGT 176

QY 851 GTCAATCTTTGACGGCAGACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGAGGTTG 910
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Db 115 TTCATCATGATCACAACAAGAAAGCGGGCTCGTTTATCACCAGTGAGAGCAGAGCTGA 56

QY 971 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1025
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Db 55 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1
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RESULT 12
US-09-232-149A-3/C
; Sequence 3, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-030-607-33

Query Match 35.2%; Score 403.2; DB 4; Length 793;
Best Local Similarity 97.1%; Pred. No. 5.7e-106;
Matches 408; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 626 GACAGACATGTTGGATGGTGAGCACCTTCTATACGACTTACAGACAGACAGATGGG 685
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QY 686 AATTGATGGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745
Db 61 AATTGATGGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 120
QY 746 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805
Db 121 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAANA 180
QY 806 AGAAGTTGCAGATGATTTGCCAAGAAGACGAAGGACAGAGTGCTGCAAAATCTTGACG 865
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QY 986 CTCTGCTGTTAAACACCCCGCATCCCTTCTTCAAAAGGATCCTTTCATAGAGAAC 1045
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RESULT 15
US-09-605-785-33
Sequence 33, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 793
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature

LOCATION: (1)...(793)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-33

Query Match 35.2%; Score 403.2; DB 4; Length 793;
Best Local Similarity 97.1%; Pred. No. 5.7e-106;
Matches 408; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 626 GACAGACATGTTGGATGGTGAGCACCTTCTATACGACTTACAGACAGACAGATGGG 685
Db 1 GACAGACATGTTGGATGGTGAGCACCTTCTATACGACTTACAGACAGACAGATGGG 60
QY 686 AATTGATGGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745
Db 61 AATTGATGGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 120
QY 746 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805
Db 121 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAANA 180
QY 806 AGAAGTTGCAGATGATTTGCCAAGAAGACGAAGGACAGAGTGCTGCAAAATCTTGACG 865
Db 181 AGAAGTTGCAGATGATTTGCCAAGAAGACGAAGGACAGAGTGCTGCAAAATCTTGACG 240
QY 866 GCACAGATGCCCTGTGTGACTCCGGTCTGACTTTTGAGAGGTTGTCATCATGATCACA 925
Db 241 GCACAGATGCCCTGTGTGACTCCGGTCTGACTTTTGAGAGGTTGTCATCATGATCACA 300
QY 926 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTGAGCCCCCGCTGCAC 985
Db 301 ACAANGAACGGGGCTCGTTTATCACCANTGAGGAGCAGACGTGAGCCCCCGCTGCAC 360
QY 986 CTCTGCTGTTAAACACCCCGCATCCCTTCTTCAAAAGGATCCTTTCATAGAGAAC 1045
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Search completed: April 2, 2003, 02:24:59
Job time : 52.0076 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 18:34:28 ; Search time 282.227 Seconds
(without alignments)
9144.390 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcattc.....ataagtaaaagctagctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1146	100.0	2005	24	AAD38603	Human alpha-methyl
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4	1142.8	99.7	1621	19	AAV61199	Full length CDNA s
5	1142.8	99.7	1621	19	AAV58584	Prostate tumour sp
6	1142.8	99.7	1621	21	AAA06347	Human immunogenic
7	1142.8	99.7	1621	22	AAS63555	Human prostate CDN
8	1142.8	99.7	1621	22	AAS10106	Human prostate tum
9	1142.8	99.7	1621	22	AAH93463	Human prostate-spe

10	1142.8	99.7	1621	22	AAH64777	Human prostate-spe
11	1142.8	99.7	1621	22	AAH02528	Prostate tumour an
12	1142.8	99.7	1621	24	ABL94927	Human F1-12 CDNA s
13	1142.8	99.7	2376	23	ABV21293	Human prostate exp
14	1142.8	99.7	2376	23	ABV21881	Human prostate exp
15	1142.8	99.7	2376	23	ABV25239	Human prostate exp
16	1142.8	99.7	2376	23	ABV27112	Human prostate exp
17	1141.2	99.6	1674	22	AAH13696	Human CDNA sequenc
18	1132	98.8	3654	24	AAD38605	Human alpha-methyl
19	1093.4	95.4	2068	24	ABK92152	Prostate cancer-as
20	932.8	81.4	1039	22	AAC91303	Human polynucleoti
21	898	78.4	1294	23	ABV22620	Human prostate exp
22	898	78.4	1294	23	ABV22733	Human prostate exp
23	898	78.4	1294	23	ABV27711	Human prostate exp
24	898	78.4	1294	23	ABV28442	Human prostate exp
25	898	78.4	1294	23	ABV28544	Human prostate exp
26	814	71.0	3023	24	AAD38606	Human alpha-methyl
27	776.8	67.8	1504	24	ABK63669	Rat sequence diffie
28	739	64.5	1317	22	AAH17637	Human CDNA sequenc
29	620.8	54.2	720	22	AAH03341	Human CDNA clone (
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31	591.8	51.6	865	23	ABV20533	Human prostate exp
32	591.8	51.6	865	23	ABV26372	Human prostate exp
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34	591.8	51.6	865	23	ABV28711	Human prostate exp
35	572.6	50.0	2012	23	ABV20131	Human prostate exp
36	572.6	50.0	2012	23	ABV20658	Human prostate exp
37	572.6	50.0	2012	23	ABV20715	Human prostate exp
38	572.6	50.0	2012	23	ABV21852	Human prostate exp
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ALIGNMENTS

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ID	AAD38603 standard; cDNA; 2005 BP.
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AC	AAD38603;
XX	
DT	23-SEP-2002 (first entry)
XX	
DE	Human alpha-methylacyl-CoA racemase SV1 CDNA #1.
XX	
KW	Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW	cytostatic; SV1; gene; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
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FT	SEQ ID NO: 3 in claim 54 of the specification"
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PN	WO200227324-A2.
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PD	04-APR-2002.
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PF	28-SEP-2001; 2001WO-US30532.
XX	
PR	28-SEP-2000; 2000US-236238P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	

PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23971.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase -
XX
PS Claim 54; Fig 1; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer, e.g. prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase SV1 cDNA.
XX
SQ Sequence 2005 BP; 519 A; 427 C; 514 G; 545 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCCGGCCTGGCCCCGGCCTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCCGGCCTGGCCCCGGCCTCTGT 125
QY 61 GCTATGCTCTCGCTGACTTCGGGGCGCGGTGTGTACGCGTGGACCGGCCGCTCCGC 120
Db 126 GCTATGCTCTCGCTGACTTCGGGGCGCGGTGTGTACGCGTGGACCGGCCGCTCCGC 185
QY 121 TACGAGCTGAGCCGCTTGGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db 186 TACGAGCTGAGCCGCTTGGGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 245
QY 181 CGGGAGCCCGCGTGTGCGGGCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240
Db 246 CGGGAGCCCGCGTGTGCGGGCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 305
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Db 366 AGGCTTATTTATGCCAGGCTGAGTGGAATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425
QY 361 GGCCAAGATATCACTATTGGCTTTGTCAAGGTGTCTCAAAAATTGGCAGAAGTGT 420
Db 426 GGCCAAGATATCACTATTGGCTTTGTCAAGGTGTCTCAAAAATTGGCAGAAGTGT 485
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
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QY 601 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGAACATGTGGATGTGGAGCACCCTTCTAT 660
Db 666 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGAACATGTGGATGTGGAGCACCCTTCTAT 725
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Db 726 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCACTTC 785
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QY 901 GAGGAGTTGTTCATCATGATCACACAAGAAAGGCGGCTGTTATCACCAGTGAAGAG 960
Db 966 GAGGAGTTGTTCATCATGATCACACAAGAAACGGGCTGTTATCACCAGTGAAGAG 1025
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAACCATCCCTTCTTC 1020
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QY 1081 CGCGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAGTAAGTAAAGCT 1140
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QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 2
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ID AAD38607 standard; cDNA; 2005 BP.
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AC AAD38607;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.
XX
KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW cytosolic; SV4; gene; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS 66..1214
FT /*tag= a
FT /product= "Human SV4 protein"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US30532.
XX
PR 28-SEP-2000; 2000US-236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23975.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA

PT	racemase	-
XX	Claim 54; Fig 9; 102pp; English.	
PS		
XX	The present invention relates to novel methods for determining whether an individual is at risk for prostate cancer or whether a prostate cancer patient is at risk for metastatic prostate cancer to the liver or lymph nodes. The method involves measuring the expression or activity of alpha-methylacyl-CoA racemase. Sequences of the invention are useful in diagnostic methods, drug screening assays, and in treating or preventing cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-acyl-CoA racemase splice variant, SV4 cDNA.	
XX	Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 other;	
SO		
	Query Match	100.0%; Score 1146; DB 24; Length 2005;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1146; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCCGGGCCGTTCTGT	60
Db	66 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCCGGGCCGTTCTGT	125
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Db	186 TAGGACGTGAGCCGCTTGGGGCGGCAAGCGCTCGTAGTGTGACCTGAACAGCCG	245
OY	181 CGGGGAGCCGCGCTGCTGCGGCGTCTGTGCAAGCGGTCGATGTCTGCTGAGCCCTC	240
Db	246 CGGGGAGCCGCGCTGCTGCGGCGTCTGTGCAAGCGGTCGATGTCTGCTGAGCCCTC	305
OY	241 CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA	300
Db	306 CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA	365
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Db	366 AGGCTTATTATGCCAGGCTGAGTTGGCCAGTCAGAACTTCTGCCGTTAGCT	425
OY	361 GGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAATTGGCAGAGTGT	420
Db	426 GGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAATTGGCAGAGTGT	485
OY	421 GAGAATCCGTAATGCCCCGCTGAATCTCCCTGCTGACTTGTGCTGCTTATGTGT	480
Db	486 GAGAATCCGTAATGCCCCGCTGAATCTCCCTGCTGACTTGTGCTGCTTATGTGT	545
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Db	546 GCACTGGCATTATATGGCTTTTGTACCCGACACGCACTGGCAAGGTCAGTCATT	605
OY	541 GATGCAAAATATGTTGGAAGAACAGCATATTAACTTTCTTGTGAAAACTCAGAAA	600
Db	606 GATGCAAAATATGTTGGAAGAACAGCATATTAACTTTCTTGTGAAAACTCAGAAA	665
OY	601 TCGAGTCTGTGGGAAGACACCTCGAGAGACATGTTGGATGGTGGAGCACCTTCTAT	660
Db	666 TCGAGTCTGTGGGAAGACACCTCGAGAGACATGTTGGATGGTGGAGCACCTTCTAT	725
OY	661 ACGACTTACAGACAGACAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC	720
Db	726 ACGACTTACAGACAGACAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC	785
OY	721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780
Db	786 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	845
OY	781 ATGGATGATTGGCCAGAAATGAAGAAGACTTTGCAGATGTATTGCAAGAAGACGAG	840

Db	846 ATGCATGATTGGCCAGAAATGAAGAAGACTTTCAGATGTATTTCGCAAGAAGACGAG	905
OY	841 GCAGATGTTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT	900
Db	906 GCAGATGTTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT	965
OY	901 GAGGAGTTGTTTCATCATGATACCAACAAGAACGGGCTCGTTTATCACCAGTGAGGAG	960
Db	966 GAGGAGTTGTTTCATCATGATACCAACAAGAACGGGCTCGTTTATCACCAGTGAGGAG	1025
OY	961 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTTTAAACACCCAGCCATCCCTCTTTC	1020
Db	1026 CAGGACGTGAGCCCCCGCCCTGCACTCTGCTTTAAACACCCAGCCATCCCTCTTTC	1085
OY	1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTTGAAGAAATTGATTGAGC	1080
Db	1086 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTTGAAGAAATTGATTGAGC	1145
OY	1081 CGGGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAAGTTAAAGCT	1140
Db	1146 CGGGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAAGTTAAAGCT	1205
OY	1141 AGTCTC 1146	
Db	1206 AGTCTC 1211	
	RESULT 3	
	AAD38604	
ID	AAD38604 standard; cDNA; 2069 BP.	
XX		
AC	AAD38604;	
XX		
DT	23-SEP-2002 (first entry)	
XX		
DE	Human alpha-methylacyl-CoA racemase SV1 cDNA #2.	
XX		
KW	Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;	
KW	cytostatic; SV1; gene; ss.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	90..1238
FT		/*tag= a
FT		/product= "Human SV1 protein #2"
XX		
PN	W0200227324-A2.	
XX		
PD	04-APR-2002.	
XX		
PF	28-SEP-2001; 2001WO-US30532.	
XX		
PR	28-SEP-2000; 2000US-236238P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Richardson J, Monahan J;	
XX		
DR	WPI; 2002-405070/43.	
DR	P-PSDB; AAE23972.	
XX		
PT	Determining risk for prostate cancer in subject or risk for metastatic prostate cancer to liver or lymph nodes of prostate cancer patients,	
PT	comprises measuring expression or activity of alpha-methylacyl-CoA	
PT	racemase	
XX		
PS	Claim 54; Fig 3; 102pp; English.	
XX		
CC	The present invention relates to novel methods for determining whether an individual is at risk for prostate cancer or whether a prostate cancer patient is at risk for metastatic prostate cancer to the liver or lymph nodes. The method involves measuring the expression or activity of	

CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
in diagnostic methods, drug screening assays, and in treating or
preventing cancer, e.g. prostate cancer. The present sequence is human
alpha-methyl-acyl-CoA racemase SV1 cDNA.

XX
SQ Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 other;

Query Match 100.0%; Score 1146; DB 24; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCGGCCCTGGCCCCGGCGCTTCTGT 60
Db 90 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCGGCCCTGGCCCCGGCGCTTCTGT 149
OY 61 GCTATGGTCTGGGCTGACTTCGGGGCGCGTGTGTACGCGGTGGACCGCGCGCTCCGC 120
Db 150 GCTATGGTCTGGGCTGACTTCGGGGCGCGTGTGTACGCGGTGGACCGCGCGCTCCGC 209
OY 121 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGCTAGTCTGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCGCTTGGGCGCGGCAAGCGCTCGCTAGTCTGACCTGAAGCAGCCG 269
OY 181 CGGGGAGCCGCGTGTGCGGGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240
Db 270 CGGGGAGCCGCGTGTGCGGGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 329
OY 241 CGCCGCGGTGTGTCATGAGAACTCCAGCTGGGCCAGAGATCTCTGACGCGGAAATCCA 300
Db 330 CGCCGCGGTGTGTCATGAGAACTCCAGCTGGGCCAGAGATCTCTGACGCGGAAATCCA 389
OY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 390 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 449
OY 361 GGGCAGCATATCAACTATTGGCTTGTGCAAGGTGTTCTCTCAAAAATTGGCAGAGTGT 420
Db 450 GGGCAGCATATCAACTATTGGCTTGTGCAAGGTGTTCTCTCAAAAATTGGCAGAGTGT 509
OY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGCTGTGGTGGCTTATGTGT 480
Db 510 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGCTGTGGTGGCTTATGTGT 569
OY 481 GCACTGGGCATTATATGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGTCAAT 540
Db 570 GCACTGGGCATTATATGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGTCAAT 629
OY 541 GATGCAATATATGTTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAACTCAGAAA 600
Db 630 GATGCAATATATGTTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAACTCAGAAA 689
OY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGATGGTGGAGCACCCTTCTAT 660
Db 690 TCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGATGGTGGAGCACCCTTCTAT 749
OY 661 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTC 720
Db 750 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTC 809
OY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGAAGTCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGAAGTCTCCCAATCAGATGAGC 869
OY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCCAAGAAGACGAAG 840
Db 870 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGATTTGCCAAGAAGACGAAG 929
OY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTCTGACTTTT 900
Db 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTCTGACTTTT 989
OY 901 GAGGAGTGTGTTCATCATGATCAACAAGGAACGGGCTGTTTATCACCAGTAGAGAG 960
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Db 990 GAGGAGTGTGTTCATCATGATCAACAAGGAACGGGCTGTTTATCACCAGTAGAGAG 1049
OY 961 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCTCTTTC 1020
Db 1050 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCTCTTTC 1109
OY 1021 AAAAGGATCTTTCATAGGAGAAACACACTGAGAGATCTTGAAGAATTGGATTCAGC 1080
Db 1110 AAAAGGATCTTTCATAGGAGAAACACACTGAGAGATCTTGAAGAATTGGATTCAGC 1169
OY 1081 CGCGAAGAGATTTATCACTTAACCTCAGATAAAAATCATTTGAAGTAAATGCTAAAAGCT 1140
Db 1170 CGCGAAGAGATTTATCACTTAACCTCAGATAAAAATCATTTGAAGTAAATGCTAAAAGCT 1229
OY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235
```

RESULT 4

AAV61199
ID AAV61199 standard; cDNA; 1621 BP.

XX AAV61199;
AC 06-JAN-1999 (first entry)
DT
XX
DE Full length cDNA sequence of prostate tumour clone F1-12.
XX
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN WO9837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-609886/51.
DR P-PSDB; AAW71867.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 76-77; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 19; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 ATGGCACTGCAGGGCATCTCGGTCGTGAGCTGTCGGCCCTGGCCCCGGCGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCATGAGCTGTCGGCCCTGGCCCCGGCGCTTCTGT 64
OY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGCGGTGAGCCGGCCGCTCCCGC 120
|||||
```

us-09-967-305-3.rng

Db 1145 AGTCTC 1150

RESULT 5
AAV58584
ID AAV58584 standard; cDNA; 1621 BP.

XX AC AAV58584;
XX DT 08-DEC-1998 (first entry)
DE Prostate tumour specific gene clone F1-12.
XX Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
OS Homo sapiens.

XX FH Location/Qualifiers
FT CDS 5..1153
FT CDS /*tag= a

PN W09837418-A2.
XX 27-AUG-1998.
XX PF 25-FEB-1998; 98WO-US03690.
XX PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-0806596.
PR 01-AUG-1997; 97US-0904809.
XX (CORI-) CORIXA CORP.
PI Dillon DC, Xu J;
XX WPI: 1998-480805/41.
DR P-PSDB; AAW69383.

PT Novel human prostate specific tumour protein and fragments - useful
PT for detecting and treating prostate cancers
XX
XX
PS Claim 1; Page 81-82; 141pp; English.

CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may
CC also be conjugated to a therapeutic agent for use in therapy of prostate
CC cancers.

XX
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 19; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCATGACAGGGGCATCTCGGTCAAGAGCTGTCCGCCCTGGCCCCGGCCGTTCTGT 60
Dy 5 ATGGCATGACAGGGGCATCTCGGTCAAGAGCTGTCCGCCCTGGCCCCGGCCGTTCTGT 64
QY 61 GCATAGTCCTGGCTACTTCGGGGCGCGCTGTGTACCGCTGGACCGGGCCGGCTCCCGC 120
Dy 65 GCTATAGTCCTGGCTACTTCGGGGCGCGCTGTGTACCGCTGGACCGGGCCGGCTCCCGC 124
QY 121 TAGCACGTGAGCCCGCTGGGGCCGGGGCAAGCGCTGCTAGTGCTGAACCTGAAGCAGCCG 180
Dy 125 TAGCACGTGAGCCCGCTGGGGCCGGGGCAAGCGCTGCTAGTGCTGAACCTGAAGCAGCCG 184
QY 181 CGGGAGCCCGCGCTGCGGGCGCTGTGCAAGCGCTGGATGTCTGCTGAGCCCTTTC 240

Db 185 CGGGAGCCGCCGCTGCTGCGCGCTCTGCAAGCGGTGAGATGCTGCTGGAGCCCTTC 244

QY 241 CGCCGGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGACGGGAAATCCA 300

Db 245 CGCCGGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGACGGGAAATCCA 304

QY 301 AGGCTATTATGCCAGGCTGAGTGAATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360

Db 305 AGGCTATTATGCCAGGCTGAGTGAATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364

QY 361 GGGCAGCATATCACTATTGGCTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420

Db 365 GGGCAGCATATCACTATTGGCTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 424

QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGCTGGTGGCTTATGTGT 480

Db 425 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGCTGGTGGCTTATGTGT 484

QY 481 GCACATGGCATTTATATGCTCTTTTGGACCGCACACGACACTGGCAAGGTCAGGTCAAT 540

Db 485 GCACATGGCATTTATATGCTCTTTTGGACCGCACACGACACTGGCAAGGTCAGGTCAAT 544

QY 541 GATGCAAAATATGCTGGAAGGAACAGCATTTTAAAGTTCTTTCTGTGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGCTGGAAGGAACAGCATTTTAAAGTTCTTTCTGTGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGCTGAGCACCTTTCTAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGCTGAGCACCTTTCTAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTGAGTGGCTGTGGAGCAATAGAACCCAGTTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGGAATTGAGTGGCTGTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784

QY 781 ATGATGATTTGGCCAGAAATGAAGAGAAGTTTGAGATGTATTGGCAAGAAGACGAAG 840

Db 785 ATGATGATTTGGCCAGAAATGAAGAGAAGTTTGAGATGTATTGGCAAGAAGACGAAG 844

QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGATCCGGTCTGACTTTT 900

Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGATCCGGTCTGACTTTT 904

QY 901 GAGAGGTTGTTCATCATGATCACAACAGGAACGGGCTGTTTATCACCACTGAGAG 960

Db 905 GAGAGGTTGTTCATCATGATCACAACAGGAACGGGCTGTTTATCACCACTGAGAG 964

QY 961 CAGGAGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020

Db 965 CAGGAGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1024

QY 1021 AAAAGGATCTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTGAGC 1080

Db 1025 AAAAGGATCTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTGAGC 1084

QY 1081 CGCGAAGAGATTATCAGCTTAACCTAGATAAAATCATTTGAAAGTAATAGTAAAGCT 1140

Db 1085 CGCGAAGAGATTATCAGCTTAACCTAGATAAAATCATTTGAAAGTAATAGTAAAGCT 1144

QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 6
ID AAA06347 standard; cDNA; 1621 BP.
XX
AC AAA06347;

XX 13-JUN-2000 (first entry)

DT Human immunogenic prostate tumour protein CDNA sequence SEQ ID NO:107.

DE Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

KW Immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN WO200004149-A2.

PD 27-JAN-2000.

XX 14-JUL-1999; 99WO-US15838.

PF 14-JUL-1998; 98US-0115453.

PR 14-JUL-1998; 98US-0116134.

PR 23-SEP-1998; 98US-0159812.

PR 23-SEP-1998; 98US-0159822.

PR 15-JAN-1999; 99US-0232149.

PR 15-JAN-1999; 99US-0232880.

PR 09-APR-1999; 99US-0288946.

XX (CORI-) CORIXA CORP.

XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

PI WPI; 2000-171268/15.

DR

XX

PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -

XX

PS Claim 1; Page 133-134; 263pp; English.

XX

CC The present invention describes isolated polypeptides, comprising an

CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides

CC and polynucleotides encoding them have cytostatic activity and can be

CC used in vaccines and in gene therapy. The polypeptides and

CC polynucleotides encoding them, antigen presenting cells which express

CC the polypeptides, antibodies against the polypeptides and vaccines

CC comprising in a patient. The polypeptides can be used to generate antibodies

CC or anti-idiotypic antibodies for passive immuno therapy. A portion of

CC the polynucleotides encoding the polypeptides can be used as a probe or

CC to modulate the expression of the polypeptides. AAA06241 to AAA0691 and

CC AY82000 to AY82020 represent sequences used in the exemplification of

CC the present invention.

XX

SEQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 21; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGAGAGCTGTCCGGCCCTGGCCCGGCTTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTCTGTGAGAGCTGTCCGGCCCTGGCCCGGCTTCTGT 64

QY 61 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTGAGAGCGGTGACCGCGGCTCCCGC 120

Db 65 GCTATGTCCTGCTGACTTGGGGCGCGTGTGTGAGAGCGGTGACCGCGGCTCCCGC 124

QY 121 TACGAGTGAGCCGCTTGGCGGGGCAAGCGCTGCTAGTGTGAGACTGAAGCAGCGC 180

Db 125 TACGAGTGAGCCGCTTGGCGGGGCAAGCGCTGCTAGTGTGAGACTGAAGCAGCGC 184

QY 181 CGGGAGCCCGCGTGTGCGCGGTCTGTGCAAGCGGTGCGATGTCTGTGAGCCCT 240

Db 185 CGGGAGCCCGCGTGTGCGCGGTCTGTGCAAGCGGTGCGATGTCTGTGAGCCCT 244

QY 241 CGCCGGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTTCTGACGGCT 300

Db 245 CGCCGGGTCATGAGAAATCCAGCTGGCCAGAGATTCGACGGGAAAAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTTGGCCAGTCAGAAAGCTTCTGCCGTTAGCT 360

Db 305 AGGCTTATTTATGCCAGGCTGAGTTGGCCAGTCAGAAAGCTTCTGCCGTTAGCT 364

QY 361 GGCCACGATATCAACTATTTGCTTTGTCAGCTGTCTCTCAAAAATTTGGCAGAGTGT 420

Db 365 GGCCACGATATCAACTATTTGCTTTGTCAGCTGTCTCTCAAAAATTTGGCAGAGTGT 424

QY 421 GAGATCCGTAATGCCCGCTGAATCTCCCTGCTGACTTTGCTGGTGGTGCCCTTATGTGT 480

Db 425 GAGATCCGTAATGCCCGCTGAATCTCCCTGCTGACTTTGCTGGTGGTGCCCTTATGTGT 484

QY 481 GCACTGGCATATTAATGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAT 540

Db 485 GCACTGGCATATTAATGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAT 544

QY 541 GATGCAATATGCTGGAAGGACAGCATATTTAAGTTCTTTCTGTGAAAACTCAGAAA 600

Db 545 GATGCAATATGCTGGAAGGACAGCATATTTAAGTTCTTTCTGTGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTTCGAGACAGACATGTTGATGTTGGAGCACCTTCTAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTTCGAGACAGACATGTTGATGTTGGAGCACCTTCTAT 664

QY 661 ACGACTTACAGACAGACAGATGGGAAATTCATGCTGTGGAGCAATAGAACCCAGTTTC 720

Db 665 ACGACTTACAGACAGACAGATGGGAAATTCATGCTGTGGAGCAATAGAACCCAGTTTC 724

QY 721 TACGAGCTGCTGATCAAAAGGACTTGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAAAGGACTTGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTTGGCCAGAAATGAAGAAGTTTGACATGATTTGCCAAAGAGACGAAG 840

Db 785 ATGGATGATTTGGCCAGAAATGAAGAAGTTTGACATGATTTGCCAAAGAGACGAAG 844

QY 841 GCAGAGTGTGTCAAATCTTTGACGGGACAGATGCTGTGACTCCGGTCTGACTTTT 900

Db 845 GCAGAGTGTGTCAAATCTTTGACGGGACAGATGCTGTGACTCCGGTCTGACTTTT 904

QY 901 GAGGAGTGTTCATCATGATCACAACAAGGAGGGGCTGTTTATCACCAAGTGAGAG 960

Db 905 GAGGAGTGTTCATCATGATCACAACAAGGAGGGGCTGTTTATCACCAAGTGAGAG 964

QY 961 CAGGACGTGAGCCCCCGCCCTGACACCTGTGCTGTTAAACACCCAGCCATCCTTCTTC 1020

Db 965 CAGGACGTGAGCCCCCGCCCTGACACCTGTGCTGTTAAACACCCAGCCATCCTTCTTC 1024

QY 1021 AAAAGGATCCTTTCATAGGAGAACACACTGAGAGAGATACTTGAAGATTGGATTGACG 1080

Db 1025 AAAAGGATCCTTTCATAGGAGAACACACTGAGAGAGATACTTGAAGATTGGATTGACG 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATTAAGSTAAAGCT 1140

Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATTAAGSTAAAGCT 1144

QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 7
AAS63555
ID AAS63555 standard; cDNA; 1621 BP.
XX AAS63555;
XX AC
XX 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #107.
XX

KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR P-PSDB; AAU69761.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 264-265; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The present sequence is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAAGGCGATCTCGGTGAGACTGTCCGGCCTGGCCCCCGGCTTCTGT 60
Db 5 ATGGCACTGCAAGGCGATCTCGGTGAGACTGTCCGGCCTGGCCCCCGGCTTCTGT 64
QY 61 GCTATGCTCTGGCTGACTTCGGGGCGCGGTGTGATGAGCGGCGGCGGCTCCGC 120
Db 65 GCTATGCTCTGGCTGACTTCGGGGCGCGGTGTGATGAGCGGCGGCGGCTCCGC 124
QY 121 TACGACGTGAGCCGCTTGCGCCGGGCAAGCGCTGCTAGTGTGAGACTGAAGCAGCG 180
Db 125 TACGACGTGAGCCGCTTGCGCCGGGCAAGCGCTGCTAGTGTGAGACTGAAGCAGCG 184
QY 181 CGGGAGCGCGCGTGTGCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGAGCGCGCGTGTGCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 244
QY 241 CGCGCGGCTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGACAGCGGAAAAATCCA 300

Db 245 CGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 304
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 305 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364
QY 361 GGCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAGAAGTGGT 420
Db 365 GGCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAGAAGTGGT 424
QY 421 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACCTTGGTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACCTTGGTGGTGGCTTATGTGT 484
QY 481 GCACTGGGCATTATTAATGGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGTCAAT 540
Db 485 GCACTGGGCATTATTAATGGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGTCAAT 544
QY 541 GATGCAATATATGTGGAAGAACACATATTTAAGTCTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAATATATGTGGAAGAACACATATTTAAGTCTTTCTGTGAAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACCTTCGAGAGACAGACATGTGGATGTGGAGCACCCTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTTCGAGAGACAGACATGTGGATGTGGAGCACCCTTCTAT 664
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCAATGGCTGTTGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGGAATTCAATGGCTGTTGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGCACTGGACTAAAGTCTGATGACTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGCACTGGACTAAAGTCTGATGACTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGAGATGATTTGCCAAAGAAGACGAG 840
Db 785 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGAGATGATTTGCCAAAGAAGACGAG 844
QY 841 GCAGAGTGGTGTCAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTCTGACTTTT 904
QY 901 GAGGAGGTGTTTCATCATGATCAACAAGAAGCGGGCTGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGGTGTTTCATCATGATCAACAAGAAGCGGGCTGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1024
QY 1021 AAAAGGATCTTTTCATAGAGAAACACACTGAGAGATCTGAAGATTGGAATTCAGC 1080
Db 1025 AAAAGGATCTTTTCATAGAGAAACACACTGAGAGATCTGAAGATTGGAATTCAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 8
AAS10106 ID AAS10106 standard; cDNA; 1621 BP.

XX AAS10106;
XX 24-OCT-2001 (first entry)
XX Human prostate tumour cDNA F1-12 #3.
DE XX

KW Human; prostate tumour protein; prostate cancer; ss.
XX Homo sapiens.
OS US6262245-B1.
PN 17-JUL-2001.
XX 25-FEB-1998; 98US-0030607.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC;
XX WPI; 2001-440862/47.
DR P-PSDB; AAU04959.
XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient
XX Claim 1; Column 112-113; 105pp; English.
XX The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
SQ
Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTGGTGTGAGAGCTGTCCGGCTGGCCCCGGCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTGGTGTGAGAGCTGTCCGGCTGGCCCCGGCCGTTCTGT 64
QY 61 GCTATGCTCTGGCTGACTTGGGGCGCGCTGTGTGTAAGCGGTGACCGCGGCTCCGC 120
Db 65 GCTATGCTCTGGCTGACTTGGGGCGCGCTGTGTGTAAGCGGTGACCGCGGCTCCGC 124
QY 121 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGACCTGAAGCAAGCCG 180
Db 125 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGACCTGAAGCAAGCCG 184
QY 181 CGGGAGCCCGCGTGTGCGCGCTCTGTGCAAGCGGTGAGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGAGCCCGCGTGTGCGCGCTCTGTGCAAGCGGTGAGATGTGCTGTGAGCCCTTC 244
QY 241 CGCGCGGTGTCATGAGAAATCTCAGCTGGGGCCAGAGATTCTGACGGGGAATTCGA 300
Db 245 CGCGCGGTGTCATGAGAAATCTCAGCTGGGGCCAGAGATTCTGACGGGGAATTCGA 304
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 305 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364
QY 361 GGCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAGAAGTGGT 420
Db 365 GGCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAGAAGTGGT 424
QY 421 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACCTTGGTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACCTTGGTGGTGGCTTATGTGT 484
QY 481 GCACTGGGCATTATTAATGGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGTCAAT 540
Db 485 GCACTGGGCATTATTAATGGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGTCAAT 544

QY 541 GATGCAATATGCTGGAGGACAGCATATTAAAGTCTTTCTGTGGAAGAACTCAGAAA 600
|||||
Db 545 GATGCAATATGCTGGAGGACAGCATATTAAAGTCTTTCTGTGGAAGAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGACATGTTGGATGGTGGAGCACCCTTCTAT 660
|||||
Db 605 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGACATGTTGGATGGTGGAGCACCCTTCTAT 664
QY 661 ACAGCTTACAGGACAGCAGATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
|||||
Db 665 ACAGCTTACAGGACAGCAGATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGATGAGC 780
|||||
Db 725 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATCCCAATCAGATGAGC 784
QY 781 ATGGATGATGGCCAGAAATGAGAAGAGTTGCAGATGTATTGCAAAAGAGACGGAAG 840
|||||
Db 785 ATGGATGATGGCCAGAAATGAGAAGAGTTGCAGATGTATTGCAAAAGAGACGGAAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCGACTTTT 900
|||||
Db 845 GCAGAGTGTGTCAAAATCTTTGACGGCAGATGCTGTGACTCCGGTTCGACTTTT 904
QY 901 GAGGAGTGTTCATCATGATCACAACAAGGAGCGGGCTGTTTATCACCAGTAGAGAG 960
|||||
Db 905 GAGGAGTGTTCATCATGATCACAACAAGGAGCGGGCTGTTTATCACCAGTAGAGAG 964
QY 961 CAGGAGCTGAGCCCCCGCCCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC 1020
|||||
Db 965 CAGGAGCTGAGCCCCCGCCCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC 1024
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGGATTGAGC 1080
|||||
Db 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGGATTGAGC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATTAATGAAATTAAGTAAAGCT 1140
|||||
Db 1085 CGCGAAGAGATTATCAGCTTAACTCAGATTAATGAAATTAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
|||||
Db 1145 AGTCTC 1150
|||||

RESULT 9
AAH93463
ID AAH93463 standard; cDNA; 1621 BP.
AC AAH93463;
XX 04-OCT-2001 (first entry)
DT 04-OCT-2001 (first entry)
XX 04-OCT-2001 (first entry)
DE Human prostate-specific full length cDNA sequence F1-12.
XX Human prostate-specific full length cDNA sequence F1-12.
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosolic; gene therapy; metastasis; ss.
XX Homo sapiens.
OS Homo sapiens.
PN WO200151633-A2.
XX 19-JUL-2001.
PD 19-JUL-2001.
XX 16-JAN-2001; 2001WO-US01574.
PF 16-JAN-2001; 2001WO-US01574.
XX 14-JAN-2000; 2000US-0483672.
PR 14-JAN-2000; 2000US-0483672.
XX (CORI-) CORIXA CORP.
PA (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 262-263; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;
Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCACTGACGAGGCAATCTGGCTGTGAGAGCTGTCCGCGCCGCGCGCTTCTGT 60
|||||
Db 5 ATGCACTGACGAGGCAATCTGGCTGTGAGAGCTGTCCGCGCCGCGCGCTTCTGT 64
QY 61 GCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGGTGAGCGCGCCGCTCCCGC 120
|||||
Db 65 GCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGGTGAGCGCGCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGCGCGGCAAGCGCTGCTAGTGTGACCTGGAACGACCG 180
|||||
Db 125 TACGACGTGAGCCGCTTGGCGCGGCAAGCGCTGCTAGTGTGACCTGGAACGACCG 184
QY 181 CGGGAGCGCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGTGCTGAGGCCCTTC 240
|||||
Db 185 CGGGAGCGCGCGCTGCTGCGCGCTGTGCAAGCGGTGCGATGTGCTGAGGCCCTTC 244
QY 241 CGCGCGGCTGTGATGAGAAACCTCAGCTGGGCCAGAGATCTGCGAGCGGGAATCCA 300
|||||
Db 245 CGCGCGGCTGTGATGAGAAACCTCAGCTGGGCCAGAGATCTGCGAGCGGGAATCCA 304
QY 301 AGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
|||||
Db 305 AGGCTTATTTATGCGAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364
QY 361 GGCCAGATATCAACTATTTGGCTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420
|||||
Db 365 GGCCAGATATCAACTATTTGGCTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 424
QY 421 GAGATCCGTAAGCCCGCTGATCTCTGCGTGAATTTGCTGTGCTGCTGCTGCTTATGTGT 480
|||||
Db 425 GAGATCCGTAAGCCCGCTGATCTCTGCGTGAATTTGCTGTGCTGCTGCTGCTTATGTGT 484
QY 481 GCACTGGGCATTTATATGCGCTTTTGGACCGCAGACGCACTGGCAAGGCTCAGTCATT 540
|||||
Db 485 GCACTGGGCATTTATATGCGCTTTTGGACCGCAGACGCACTGGCAAGGCTCAGTCATT 544
QY 541 GATGCAATATGCTGGAGGAGACAGCATATTTAAGTCTTTCTGTGGAAGAACTCAGAAA 600
|||||
Db 545 GATGCAATATGCTGGAGGAGACAGCATATTTAAGTCTTTCTGTGGAAGAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGACATGTTGGATGGTGGAGCACCCTTCTAT 660
|||||
Db 605 TCGAGTCTGTGGGAAGCACCCTCGAGGACAGACATGTTGGATGGTGGAGCACCCTTCTAT 664

QY	661	ACGACTTACAGGACAGACAGATGGGGGAATTCAATGCGCTGTTGGAGCAATAGAACCCACAGTTC	720
Db	665	ACGACTTACAGGACAGACAGATGGGGGAATTCAATGCGCTGTTGGAGCAATAGAACCCACAGTTC	724
QY	721	TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	780
Db	725	TACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	784
QY	781	ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATCTATTTCGAAAGAAAGACGAG	840
Db	785	ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATCTATTTCGAAAGAAAGACGAG	844
QY	841	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT	900
Db	845	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTACTCCGGTCTGACTTTT	904
QY	901	GAGGAGGTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTATCACCAGTGAGGAG	960
Db	905	GAGGAGGTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTATCACCAGTGAGGAG	964
QY	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC	1020
Db	965	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC	1024
QY	1021	AAAAAGGATCCTTTCATATAGGAGAACAACACTGAGGAGATACCTTGAAGAATTGGATTTCAGC	1080
Db	1025	AAAAAGGATCCTTTCATATAGGAGAACAACACTGAGGAGATACCTTGAAGAATTGGATTTCAGC	1084
QY	1081	CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATTAAGTTAAAAAGCT	1140
Db	1085	CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATTAAGTTAAAAAGCT	1144
QY	1141	AGTCTC 1146	
Db	1145	AGTCTC 1150	

RESULT	10
AAH84777	
ID	AAH84777 standard; cDNA; 1621 BP.
XX	
AC	AAH84777;
XX	
DT	25-SEP-2001 (first entry)
XX	
DE	Human prostate-specific cDNA sequence F1-12/P504S.
XX	
KW	Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW	chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW	prostate specific antigen; PSA; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200134802-A2.
XX	
PD	17-MAY-2001.
XX	
PF	09-NOV-2000; 2000WO-US30904.
XX	
PR	12-NOV-1999; 99US-0439313.
PR	18-NOV-1999; 99US-0443686.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX	
DR	WPI; 2001-308785/32.
XX	
PT	Isolated polypeptide comprising at least an immunogenic portion of a
PT	prostate-specific protein, useful in the diagnosis and therapy of
PT	prostate cancer -

Query Match	Best Local Similarity	Score	Pred.	Mismatches	Indels	Gaps	Length
99.7%;	99.8%;	1142.8;	DB 22;	0;	0;	0;	1621;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;							
1	ATGGCACTGCAGGGCATCTCGCTGAGAGCTGTCCGGCTGGCCCGGGCGTTCTGT	60					
5	ATGGCACTGCAGGGCATCTCGCTGAGAGCTGTCCGGCTGGCCCGGGCGTTCTGT	64					
61	GCATAGTCTCGCTGACTTCGGGGGGCGTGTGTACGCGTGAACGGCCGGCTCCGC	120					
65	GCATAGTCTCGCTGACTTCGGGGGGCGTGTGTACGCGTGAACGGCCGGCTCCGC	124					
121	TACGACGTGAGCCGCTTGGGGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG	180					
125	TACGACGTGAGCCGCTTGGGGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG	184					
181	CGGGGAGCCCGCGTGTGCGCGCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC	240					
185	CGGGGAGCCCGCGTGTGCGCGCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC	244					
241	CGCGCGCGTGTGATGAGAACTCCAGCTGGGGCCAGAGATTCTGACGCGGAAATCCA	300					
245	CGCGCGCGTGTGATGAGAACTCCAGCTGGGGCCAGAGATTCTGACGCGGAAATCCA	304					
301	AGGCTATTATGACGAGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360					
305	AGGCTATTATGACGAGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	364					
361	GGCCACGATATCAACTATTGGCTTTGTACAGGTGTTCTCTCAAAATTGGCAGAAAGTGT	420					
365	GGCCACGATATCAACTATTGGCTTTGTACAGGTGTTCTCTCAAAATTGGCAGAAAGTGT	424					
421	GAGATCCGATATGCCCCCGCTGAATCTCTGGCTGACTTTGCTGTGTGGCCTTATGTGT	480					
425	GAGATCCGATATGCCCCCGCTGAATCTCTGGCTGACTTTGCTGTGTGGCCTTATGTGT	484					
481	GCACTGGGCATTATATAGGCTCTTTTGAACCGCACACGCACTGGCAAGGGTCAGGTCAAT	540					
485	GCACTGGGCATTATATAGGCTCTTTTGAACCGCACACGCACTGGCAAGGGTCAGGTCAAT	544					
541	GATGCAATATATGTTGGAAGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA	600					
545	GATGCAATATATGTTGGAAGAACACATATTTAAGTCTTTTCTGTGAAAACTCAGAAA	604					
601	TGCACTCTGTGGAAGACACCTCGAGAGACAGAACATGTTGATGGTGAGCACCTTCTAT	660					
605	TGCACTCTGTGGAAGACACCTCGAGAGACAGAACATGTTGATGGTGAGCACCTTCTAT	664					
661	ACCACTTACAGGACAGACATGGGGAATTCATGGCTGTGGAGCAATAGAACCAGTTC	720					
665	ACCACTTACAGGACAGACATGGGGAATTCATGGCTGTGGAGCAATAGAACCAGTTC	724					
721	TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCATCAGATGAGC	780					
725	TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCATCAGATGAGC	784					

QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTCAAAGAAGACGAAG 840
Db 785 ATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTCAAAGAAGACGAAG 844
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCCCTGTGTGACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCCCTGTGTGACTCCGGTCTGACTTTT 904
QY 901 GAGAGGTTGTCATCATGATCACAACAAGGAACGGGGCTGTTTATCACAGTAGAGAG 960
Db 905 GAGAGGTTGTCATCATGATCACAACAAGGAACGGGGCTGTTTATCACAGTAGAGAG 964
QY 961 CAGAGCGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTTTC 1020
Db 965 CAGAGCGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTTTC 1024
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGATTGATTCAGC 1080
Db 1025 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGATTGATTCAGC 1084
QY 1081 CGCGAAGAGATTTCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 11
AAH02528 standard; cDNA; 1621 BP.

AC AAH02528;

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen determined full length cDNA sequence for F1-12.

KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;

KW prostate cancer; immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN WO200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US27464.

PR 04-OCT-1999; 99US-0157455.

PA (CORI-) CORIXA CORP.

PI Xu J, Skeiky YAW, Reed SG, Cheever MA;

DR WPI; 2001-245062/25.

DR P-PSDB; AAB74798.

PT Prostate specific protein and its encoding polynucleotide, useful for
the treatment and diagnosis of prostate cancer -

PS Claim 4; Page 153; 276pp; English.

XX The present invention describes an isolated polypeptide (I) comprising
at least an immunogenic portion of a prostate tumour antigen protein or
its variant. (I) have cytostatic activity and can be used in vaccine
production. (I), prostate tumour antigen polynucleotides, an antigen
presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
pharmaceutical composition containing (I) are useful for inhibiting the
development of cancer in a patient. Antibodies specific for prostate
specific proteins and oligonucleotides that hybridise to a

CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.

XX Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 22; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCCTGGCCCCCGGCGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCCTGGCCCCCGGCGCTTCTGT 64
QY 61 GCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTACGGGTGACCGCGCGCTCCGC 120
Db 65 GCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTGTACCGCGCGCTCCGC 124
QY 121 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGTACTGTGAGCTGAAGACGCC 180
Db 125 TACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGTACTGTGAGCTGAAGACGCC 184
QY 181 CGGGAGCCCGCGTGTCTCGGGCGGTGTGCAAGCGGTGATGTGTGAGCCCTTC 240
Db 185 CGGGAGCCCGCGTGTCTCGGGCGGTGTGCAAGCGGTGATGTGTGAGCCCTTC 244
QY 241 CGCCCGCGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db 245 CGCCCGCGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 304
QY 301 AGGCTATTATGAGCCAGCTGAGTGTGATTTGGCCAGTCAAGAACTTCCCGGTAGCT 360
Db 305 AGGCTATTATGAGCCAGCTGAGTGTGATTTGGCCAGTCAAGAACTTCCCGGTAGCT 364
QY 361 GGGCAGCATATCAACTATTGGCTTTGTACAGGTGTTCTCAAAAATTTGGCAGAAGTGT 420
Db 365 GGGCAGCATATCAACTATTGGCTTTGTACAGGTGTTCTCAAAAATTTGGCAGAAGTGT 424
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGTGTGTGGCTTATGTGT 480
Db 425 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGTGTGTGGCTTATGTGT 484
QY 481 GCACGTGGCATTTAATAGGCTCTTTTTCAGCCGACAGCAGCTGGCAAGGCTCAGTCAAT 540
Db 485 GCACGTGGCATTTAATAGGCTCTTTTTCAGCCGACAGCAGCTGGCAAGGCTCAGTCAAT 544
QY 541 GATGCAATATGTTGGAAGAACAGCATTTTAAGTCTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAATATGTTGGAAGAACAGCATTTTAAGTCTTTCTGTGAAAACTCAGAAA 604
QY 601 TCGAGTCTGGGAAGCACTCGAGAGCAAAATGTTGATGTTGAGGACCTTTCTAT 660
Db 605 TCGAGTCTGGGAAGCACTCGAGAGCAAAATGTTGATGTTGAGGACCTTTCTAT 664
QY 661 ACGACTTACAGGACAGCATGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCATGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTCAAAGAAGACGAAG 840
Db 785 ATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTCAAAGAAGACGAAG 844
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCCCTGTGTGACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAAAATCTTTGACGGCAGAGATGCCCTGTGTGACTCCGGTCTGACTTTT 904
QY 901 GAGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTGTTTATCACCAAGTAGAGAG 960

Db 905 GAGGAGCTGTTTCATCATGATCACAACAAGAACGGGGCTGTTTATCACCAGTAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTCTTC 1024
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGGAGATCTTGAAGATTGGATTGAC 1080
Db 1025 AAAAGGATCCTTTCATAGAGAACACACTGAGGAGATCTTGAAGATTGGATTGAC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 12
ABL94927
ID ABL94927 standard; cDNA; 1621 BP.
AC ABL94927;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human FI-12 cDNA sequence SEQ ID NO 107.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
PS Claim 1; SEQ ID NO 107; 87bp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 24; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGCTGCTGAGAGCTGTCCGGCCCTGGCCCCGGCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGCTGCTGAGAGCTGTCCGGCCCTGGCCCCGGCCGTTCTGT 64
QY 61 GCTATGCTCCTGGCTGACTTCGGGGGGGGCGGTGTGTACGGCTGAGACCGGCCGCTCCCGC 120
Db 65 GCTATGCTCCTGGCTGACTTCGGGGGGGGCGGTGTGTGTACGGCTGAGACCGGCCGCTCCCGC 124
QY 121 TAGCAGCTGAGCCGCTTGGGGGGGGGCAAGCGCTCGCTAGTCTGAGCCTGAAGACGCCG 180
Db 125 TAGCAGCTGAGCCGCTTGGGGGGGGGCAAGCGCTCGCTAGTCTGAGCCTGAAGACGCCG 184
QY 181 CGGGAGCCCGCCGCTGCTCGGGCGTCTGTGCAAGCGGCTCGATGTGCTGAGACCCCTTC 240
Db 185 CGGGAGCCCGCCGCTGCTCGGGCGTCTGTGCAAGCGGCTCGATGTGCTGAGACCCCTTC 244
QY 241 CGCCGGGGGTGTCATGAGAAACTCCAGCTGGGGCCAGAGATTCTGACGGGGGAAATCCA 300
Db 245 CGCCGGGGGTGTCATGAGAAACTCCAGCTGGGGCCAGAGATTCTGACGGGGGAAATCCA 304
QY 301 AGGCTTATTATGCCAGGCTGAGTGATTTGGCCAGTCAAGAAAGCTTCTGCGGTTAGCT 360
Db 305 AGGCTTATTATGCCAGGCTGAGTGATTTGGCCAGTCAAGAAAGCTTCTGCGGTTAGCT 364
QY 361 GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCAAAAATTGGCAGAAAGTGT 420
Db 365 GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCAAAAATTGGCAGAAAGTGT 424
QY 421 GAGAAATCCGATGCCCCCGCTGAATCTCTGCGTGAATTTGCTGCTGCTGCTGCTGCT 480
Db 425 GAGAAATCCGATGCCCCCGCTGAATCTCTGCGTGAATTTGCTGCTGCTGCTGCTGCT 484
QY 481 GCACTGGGCATTATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCATT 540
Db 485 GCACTGGGCATTATATGCTCTTTTGGACCGCACAGCACTGGCAAGGGTCAAGTCATT 544
QY 541 GATGCAATATATGTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCAGAAA 600
Db 545 GATGCAATATATGTGGAAGAACAGCATATTTAAGTTCTTTCTGTGGAAGAACTCAGAAA 604
QY 601 TCGAGTCTGTGGAGACACCTCGAAGACAGACAGACATGTTGATGCTGGAGCACCTTCTAT 660

|||||
Db 605 TCGAGTCTGTGGGAGCACCCTCGAGACAGAAACATGTGGATGGTGAGCACCCTTCTAT 664
QY 661 ACGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGGACTTGAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGGACTTGAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTGGCAAGAAGACGAAAG 840
Db 785 ATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTGGCAAGAAGACGAAAG 844
QY 841 GCAGAGTGTGTCAAAATCTTTGACGCGACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAAATCTTTGACGCGACAGATGCTGTGACTCCGGTCTGACTTTT 904
QY 901 GAGAGGTTGTTCAATCATGATCACACAAGGAGGCGCTGTTTATCACCAGTGAGGAG 960
Db 905 GAGAGGTTGTTCAATCATGATCACACAAGGAGGCGCTGTTTATCACCAGTGAGGAG 964
QY 961 CAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCGCATCCCTTCTTTC 1020
Db 965 CAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCGCATCCCTTCTTTC 1024
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTGAAGAATTTGGATTGAGC 1080
Db 1025 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTGAAGAATTTGGATTGAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAAATGAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAAATGAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 13
ABV21293
ID ABV21293 standard; cDNA; 2376 BP.
XX
AC ABV21293;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21284.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.

XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 3532; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
Query Match 99.7%; Score 1142.8; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCACTGACAGGCGATCTCGTGTGAGAGCTGTCGGCCCGCCGCGTCTGT 60
Db 101 ATGCACTGACAGGCGATCTCGTGTGAGAGCTGTCGGCCCGCCGCGTCTGT 160
QY 61 GCTATGCTCCTGGCTGACTTCGGGGCGCGGTGTGTAACCGGACCGGCTCCGC 120
Db 161 GCTATGCTCCTGGCTGACTTCGGGGCGCGGTGTGTAACCGGACCGGCTCCGC 220
QY 121 TACGAGCTGAGCCGCTTGGCGCGGGCAAGCGCTGCTAGCTGAGACGACCGG 180
Db 221 TACGAGCTGAGCCGCTTGGCGCGGGCAAGCGCTGCTAGCTGAGACGACCGG 280
QY 181 CGGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 240
Db 281 CGGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTGATGTGCTGTGAGCCCTTC 340
QY 241 CGCCGCGGTGTCAATGAGAAATCCAGCTGGGCGGACAGATCTGCAGCGGAAATCCA 300
Db 341 CGCCGCGGTGTCAATGAGAAATCCAGCTGGGCGGACAGATCTGCAGCGGAAATCCA 400
QY 301 AGGCTTATTTATGCCAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 360
Db 401 AGGCTTATTTATGCCAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 460
QY 361 GGCCACGATATCACTATTTGGCTTGTGACAGTGTCTCTCAAAATTTGGCAGAGTGT 420
Db 461 GGCCACGATATCACTATTTGGCTTGTGACAGTGTCTCTCAAAATTTGGCAGAGTGT 520
QY 421 GAGATCCGTATGCCCGCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT 480
Db 521 GAGATCCGTATGCCCGCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT 580
QY 481 GCACTGGGCAATTAATGCGCTTTTGTGACCGGACAGCGCACTGGCAAGGTCAGTCAAT 540
Db 581 GCACTGGGCAATTAATGCGCTTTTGTGACCGGACAGCGCACTGGCAAGGTCAGTCAAT 640
QY 541 GATGCAATATGTTGGGAAGAACAGCATATTTAAGTCTCTTGTGTGAAAACTCAGAAA 600
Db 641 GATGCAATATGTTGGGAAGAACAGCATATTTAAGTCTCTTGTGTGAAAACTCAGAAA 700
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGCTGAGACCTTCTAT 660
Db 701 TCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGCTGAGACCTTCTAT 760

QY 661 ACGACTTACAGACAGACAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACCCAGTTC 720
DB 761 ACGACTTACAGACAGACAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACCCAGTTC 820
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
DB 821 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 880
QY 781 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGCAGATGATTTGCAAGAAGACGGAAG 840
DB 881 ATGATGATTTGGCCAGAAATGAGAAGAGTTTGCAGATGATTTGCAAGAAGACGGAAG 940
QY 841 GCAGAGTGTGTCATAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT 900
DB 941 GCAGAGTGTGTCATAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT 1000
QY 901 GAGAGGTTGTTCATCATGATCACAACAAGGAGCGGGCTCGTTATACACAGTGAGGAG 960
DB 1001 GAGAGGTTGTTCATCATGATCACAACAAGGAGCGGGCTCGTTATACACAGTGAGGAG 1060
QY 961 CAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTCTTTC 1020
DB 1061 CAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTCTTTC 1120
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTACGC 1080
DB 1121 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTACGC 1180
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATGTAAGGCT 1140
DB 1181 CGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAATGTAAGGCT 1240
QY 1141 AGTCTC 1146
DB 1241 AGTCTC 1246

RESULT 14
ABV21881
ID ABV21881 standard; cDNA: 2376 BP.
AC ABV21881;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 21872.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 3719; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
Query Match 99.7%; Score 1142.8; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGCTCGTGAGCTGCCGGCTGGCCCCCGGCGTCTGT 60
DB 101 ATGGCACTGCAGGGCATCTCGCTCGTGAGCTGCCGGCTGGCCCCCGGCGTCTGT 160
QY 61 GCTATGTCCTGCTGACTTCGGGGCGCGTGTGTACGCGTGAGCGGGCGCTCCGC 120
DB 161 GCTATGTCCTGCTGACTTCGGGGCGCGTGTGTACGCGTGAGCGGGCGCTCCGC 220
QY 121 TACGACGTGACCGCCTTGGCCGGGCGAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
DB 221 TACGACGTGACCGCCTTGGCCGGGCGAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 280
QY 181 CGGGAGCCCGCTGCTGCGCGCTGTGCAAGCGGTGATGCTGCTGAGCCCTTC 240
DB 281 CGGGAGCCCGCTGCTGCGCGCTGTGCAAGCGGTGATGCTGCTGAGCCCTTC 340
QY 241 CGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
DB 341 CGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 400
QY 301 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
DB 401 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 460
QY 361 GGCCACGATATCAACTATTGCGCTTGTGAGGTCTCTCAAAAATTGGCAGAAGTGT 420
DB 461 GGCCACGATATCAACTATTGCGCTTGTGAGGTCTCTCAAAAATTGGCAGAAGTGT 520
QY 421 GAGAATCCGTAATGCCCCGCTGAATCTCCTGCGTACTTTGCTGCTGCTGCTTATGTGT 480
DB 521 GAGAATCCGTAATGCCCCGCTGAATCTCCTGCGTACTTTGCTGCTGCTGCTTATGTGT 580
QY 481 GCACCTGGCATTAATATGCTCTTTTGACCCGACACGCACTGGCAAGGTCAGTCAAT 540
DB 581 GCACCTGGCATTAATATGCTCTTTTGACCCGACACGCACTGGCAAGGTCAGTCAAT 640
QY 541 GATGCAAAATATGTTGGAAGGAACAGCATTTTAAGTCTTTCTGTGGAATACTCAGAAA 600
DB 641 GATGCAAAATATGTTGGAAGGAACAGCATTTTAAGTCTTTCTGTGGAATACTCAGAAA 700
QY 601 TCGAGTCTGTGGAAACACCTCGAGGACAGAAATGTTGATGCTGAGCACCCTTCTAT 660
DB 701 TCGAGTCTGTGGAAACACCTCGAGGACAGAAATGTTGATGCTGAGCACCCTTCTAT 760
QY 661 ACGACTTACAGACAGACAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACCCAGTTC 720
DB 761 ACGACTTACAGACAGACAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACCCAGTTC 820

QY 721 TACGACCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
|||||
Db 821 TACGAGCTGCTGATCAAAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 880
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCCAAAGAAGACGAAG 840
|||||
Db 881 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCCAAAGAAGACGAAG 940
QY 841 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
|||||
Db 941 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 1000
QY 901 GAGGAGCTTGTTCATCATGATCACAAAGAAGCGGGCTCGTTTATCACCAGTGAGGAG 960
|||||
Db 1001 GAGGAGCTTGTTCATCATGATCACAAAGAAGCGGGCTCGTTTATCACCAGTGAGGAG 1060
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
|||||
Db 1061 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1120
QY 1021 AAAAGGATCCTTTCATAGGAGACACACTGAGGAGATCTTGAAGAATTTGATTCAGC 1080
|||||
Db 1121 AAAAGGATCCTTTCATAGGAGACACACTGAGGAGATCTTGAAGAATTTGATTCAGC 1180
QY 1081 CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAATTCATTGAAGTAAATGATTAAGCT 1140
|||||
Db 1181 CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAATTCATTGAAGTAAATGATTAAGCT 1240
QY 1141 AGTCTC 1146
|||||
Db 1241 AGTCTC 1246

RESULT 15
ABV25239
ID ABV25239 standard; cDNA; 2376 BP.
XX
AC ABV25239;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25230.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4947-4948; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;

Query Match 99.7%; Score 1142.8; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGACAGGCGATCTCGTTCGTGAGCTGTCCGGCCCGCCCGCTTCTGT 60
|||||
Db 101 ATGGCACTGACAGGCGATCTCGTTCGTGAGCTGTCCGGCCCGCCCGCTTCTGT 160
QY 61 GCTATGTCCTGCTGACTTCGCGCGCGCTGTGTGACGCGTGACCGCGCCGCTCCCGC 120
|||||
Db 161 GCTATGTCCTGCTGACTTCGCGCGCGCTGTGTGACGCGTGACCGCGCCGCTCCCGC 220
QY 121 TACGACGTGAGCCGCTTGGCGCGGGCAAGCCGCTGCTAGTCTGAGCCTGAAGCAGCCG 180
|||||
Db 221 TACGACGTGAGCCGCTTGGCGCGGGCAAGCCGCTGCTAGTCTGAGCCTGAAGCAGCCG 280
QY 181 CGCGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGCTGCTGAGCCCTTC 240
|||||
Db 281 CGCGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGCTGCTGAGCCCTTC 340
QY 241 CGCGCGGCTGTGATGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAATCCA 300
|||||
Db 341 CGCGCGGCTGTGATGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAATCCA 400
QY 301 AGGCTTATTTATGCCAGGCTGATGATTTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
|||||
Db 401 AGGCTTATTTATGCCAGGCTGATGATTTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 460
QY 361 GGCACGATATCACTATTTGGCTTGTCTCAGGTGTTCTCTCAAAATTTGGCAGAAGTGT 420
|||||
Db 461 GGCACGATATCACTATTTGGCTTGTCTCAGGTGTTCTCTCAAAATTTGGCAGAAGTGT 520
QY 421 GAGATCCGATGCCCCCGCTGATCTCTGCTGACTTGTGCTGCTGCTGCTATGTGT 480
|||||
Db 521 GAGATCCGATGCCCCCGCTGATCTCTGCTGACTTGTGCTGCTGCTGCTATGTGT 580
QY 481 GCACTGGCATTTATATGCTTTTGGACCGCACAGCAGCTGCAAGGGTCAAGTCAAT 540
|||||
Db 581 GCACTGGCATTTATATGCTTTTGGACCGCACAGCAGCTGCAAGGGTCAAGTCAAT 640
QY 541 GATGCAATATGTTGGAAGGAGACGATATTTAAGTCTTTCTGTGGAATACTCAGAAA 600
|||||
Db 641 GATGCAATATGTTGGAAGGAGACGATATTTAAGTCTTTCTGTGGAATACTCAGAAA 700
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGGTGAGACACTTCTAT 660
|||||
Db 701 TCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGGTGAGACACTTCTAT 760
QY 661 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720
|||||
Db 761 ACGACTTACAGACAGCAGATGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 820
QY 721 TACGAGCTGCTGATCAAGGAGCTTGAGCTAAAGTCTGATGAGCTTCCCAATCAGATGAGC 780
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Db 821 TACGAGCTGCTGATCAAGGACTTGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 880
QY 781 ATGGATGATGGCCAGAAATGAAGAAGAGTTCAGATGTATTTGCAAGAAGACGAAG 840
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 881 ATGGATGATGGCCAGAAATGAAGAAGAGTTCAGATGTATTTGCAAGAAGACGAAG 940
QY 841 GCAGAGTGGTCAAAATCTTTGACGGGACAGATGCCCTGTGTGACTCCGGTCTGACTTTT 900
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 941 GCAGAGTGGTCAAAATCTTTGACGGGACAGATGCCCTGTGTGACTCCGGTCTGACTTTT 1000
QY 901 GAGGAGTGGTTCATCATGATGATCACAAGAAAGGGGCTCGTTTATCACCAGTGAGGAG 960
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1001 GAGGAGTGGTTCATCATGATGATCACAAGAAAGGGGCTCGTTTATCACCAGTGAGGAG 1060
QY 961 CAGGAGTGAAGCCCCCGCCCTGACACCTCTGCTTAACACACCCAGCCATCCCTTCTTC 1020
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1061 CAGGAGTGAAGCCCCCGCCCTGACACCTCTGCTTAACACACCCAGCCATCCCTTCTTC 1120
QY 1021 AAAAGGATCCCTTCATAGAGAACACACTGAGAGATCTGAAGAATTTGGATTTCAGC 1080
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1121 AAAAGGATCCCTTCATAGAGAACACACTGAGAGATCTGAAGAATTTGGATTTCAGC 1180
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATGAAGCT 1140
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Db 1181 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAAATGAAGCT 1240
QY 1141 AGTCTC 1146
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Db 1241 AGTCTC 1246

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Search completed: April 1, 2003, 19:55:07
 Job time : 285.227 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on:      April 1, 2003, 19:42:24 ; Search time 3415.69 Seconds
              (without alignments)
              9506.702 Million cell updates/sec
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Title: US-09-967-305-1
 Perfect score: . 2005
 Sequence: 1 ttgcagcgtcgtcgtgctgg.....acatccagaataaagttct 2005

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	957.6	47.8	1010	9	AL580638	AL580638
	2	944.2	47.1	968	9	AL558928	AL558928
	3	907	45.2	959	9	AL575193	AL575193
c	4	852.2	42.5	888	9	AL558977	AL558977
	5	850.4	42.4	955	12	BG741165	BG741165
	6	846.2	42.2	873	9	AL555978	AL555978

C	7	826.2	41.2	838	9	AL571115	AL571115	AL571115
C	8	815.8	40.7	842	9	AL551698	AL551698	AL551698
	9	813.6	40.6	823	14	BM723657	BM723657	UI-E-EJ0-
	10	810.6	40.4	1523	11	AK002401	AK002401	Mus muscu
	11	796.4	39.7	824	9	AL545355	AL545355	AL545355
	12	781.8	39.0	820	14	BQ962523	BQ962523	AGENCOURT
	13	728	36.3	890	14	BQ941482	BQ941482	AGENCOURT
	14	720.6	35.7	808	13	BI256255	BI256255	602975075
C	15	715.8	35.9	763	9	AL580686	AL580686	AL580686
C	16	705.4	35.2	880	12	BG289921	BG289921	602381336
C	17	700.8	35.0	792	12	BG432394	BG432394	602495424
C	18	695.2	34.7	740	14	BM675180	BM675180	UI-E-EJ0-
C	19	685.8	34.2	720	9	AL117376	AL117376	AL117376
C	20	684.4	34.1	712	9	AI796120	AI796120	wh42f03.x
	21	674.6	33.6	935	12	BG286300	BG286300	602382457
	22	672.4	33.5	748	9	AL126425	AL126425	AL126425
	23	665.6	33.2	672	14	BM714377	BM714377	UI-E-EJ0-
	24	664.6	33.1	943	12	BG289079	BG289079	602383954
C	25	660.8	33.0	687	9	AI1373634	AI1373634	qz53d12.x
	26	659.8	32.9	812	12	BG035606	BG035606	602325670
	27	654.2	32.6	693	12	BG779839	BG779839	x02667316
C	28	644	32.1	654	10	AM271287	AM271287	x946a08.x
	29	640	31.9	649	14	BQ638373	BQ638373	hd21g09.y
C	30	639.6	31.9	726	10	AM242775	AM242775	xm89f06.x
C	31	639.4	31.9	681	14	BQ009670	BQ009670	UI-H-ED1-
	32	637.6	31.8	916	12	BG167682	BG167682	602342867
	33	635.6	31.7	875	12	BE869129	BE869129	601445110
C	34	633.8	31.6	729	13	BI550368	BI550368	603192419
C	35	626	31.2	636	9	AA779728	AA779728	af44b01.s
C	36	626	31.2	647	12	BF062030	BF062030	7k70f07.x
C	37	623.8	31.1	658	10	BE218541	BE218541	hv41b10.x
C	38	605.8	30.2	713	10	AV714764	AV714764	AV714764
	39	570.6	28.5	937	12	BG165573	BG165573	602343724
	40	569	28.4	914	12	BF796706	BF796706	602258327
	41	567.8	28.3	690	12	BF205467	BF205467	601867855
C	42	565.8	28.2	599	12	BF857744	BF857744	QV1-FT020
C	43	563	28.1	590	10	AM965831	AM965831	EST377904
	44	557.2	27.8	701	10	BE298582	BE298582	601119742
	45	555.6	27.7	938	10	BE622419	BE622419	601441213

ALIGNMENTS

RESULT 1	AL580638/c	1010 bp	mRNA	linear	EST 16-FEB-2001
LOCUS	AL580638	LTI_NFL008_TC2	Homo sapiens	cDNA clone CS0DJ007YI07 3	
DEFINITION	AL580638	prime, mRNA sequence.			
ACCESSION	AL580638				
VERSION	AL580638.1	GI:12946852			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	unpublished (2001)				
COMMENT	Contact: Genoscope				

FEATURES

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/sex="male"
/tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA"

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was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 304 a 199 c 198 g 307 t 2 others
ORIGIN

Query Match 47.8%; Score 957.6; DB 9; Length 1010;
Best Local Similarity 98.98; Pred. No. 3.1e-239;
Matches 994; Conservative 1; Mismatches 6; Indels 4; Gaps 3;

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Db 943 CCTGCACCTCTGCTG-TAAACACCCCGCATCCCTTCTTCAAAAGGATCCTTCATA 885

QY 1104 GGAGAACACACTGAGAGATCTGAAGAATTGGATTCAAGCCGGAAGAGATTATCAG 1163
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Db 884 GGAGAACACACTGAGAGATCTGAAGAATTGGATTCAAGCCGGAAGAGATTATCAG 825

QY 1164 CTTAACTCAGATAAAATCATTTGAAGTAATAGGTAAGCTAGTCTTAACCTCCAGGC 1223
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Db 824 CTTAACTCAGATAAAATCATTTGAAGTAATAGGTAAGCTAGTCTTAACCTCCAGGC 765

QY 1224 CCACGGCTCAAGTAATTGAATACTGCATTTACAGTGAAGTAACACATTAACATTGTA 1283
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Db 764 CCACGGCTCAAGTAATTGAATACTGCATTTACAGTGAAGTAACACATTAACATTGTA 705

QY 1284 TGCATGGAACATGAGGAGACGTATTACAGTGTCTTACACACTCTAATCAAGAAAAGAT 1343
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Db 704 TGCATGGAACATGAGGAGACGTATTACAGTGTCTTACACACTCTAATCAAGAAAAGAT 645

QY 1344 TACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAAGTGTATCATTTAGGCTTTT 1403
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Db 644 TACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAAGTGTATCATTTAGGCTTTT 585

QY 1404 GATTTATAAACTTTGGTACTTATACTAAATATGTAGTATTCTGCCCTCCAGTTTG 1463
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Db 584 GATTTATAAACTTTGGTACTTATACTAAATATGTAGTATTCTGCCCTCCAGTTTG 525

QY 1464 CTTGATATATTGTTGATATTAAGATTCTTGACTTATATTTTGAATGGGTTCTAGTGA 1523
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Db 524 CTTGATATATTGTTGATATTAAGATTCTTGACTTATATTTTGAATGGGTTCTAGTGA 465

QY 1524 AAGGAATGATATATTCTGAAGACATCGATATACATTTTACACTCTTGATTTACAA 1583
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Db 464 AAGGAATGATATATTCTGAAGACATCGATATACATTTTACACTCTTGATTTACAA 405

QY 1584 TGTAGAAAATGAGGAAATGCCACAATTTGTATGTGTGAATAAGTCACGTGAACAGAGTG 1643
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Db 404 TGTAGAAAATGAGGAAATGCCACAATTTGTATGTGTGAATAAGTCACGTGAACAGAGTG 345

QY 1644 ATTGGTTGCATCCAGGCTTTTGTCTGTGTTGATCTCCCTTAAGCACATTTCAA 1703
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Db 344 ATTGGTTGCATCCAGGCTTTTGTCTGTGTTGATCTCCCTTAAGCACATTTCAA 285

QY 1704 ACTTTAGCAACAGTTATACACTTTGTAATTGCAAGAAAAGTTTACCTGTATGTAAT 1763
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Db 284 ACTTTAGCAACAGTTATACACTTTGTAATTGCAAGAAAAGTTTACCTGTATGTAAT 225

QY 1764 CAGAATGCTTCAACTGAAAAAATATCCAAAAATAGAGAAATGTGTGCTCACT 1823
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Db 224 CAGAATGCTTCAACTGAAAAAATATCCAAAAATAGAGAAATGTGTGCTCACT 165

QY 1824 ACGTAGAGTCCAGAGGACAGTCACTTTTAGGGTGCCTGATCCAGTAACCTGGGGCT 1883

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Db 164 ACGTAGAGTCCAGAGGACAGTCACTTTTAGGGTGCCTGATCCAGTAACCTGGGGCT 105

QY 1884 GTTCCCGCTGGGCTCTGGGCTGTACGCTTTCTTCATGATGTTGATTTCTCTC 1943
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Db 104 GTTCCCGCTGGGCTCTGGGCTGTACGCTTTCTTCATGATGTTGATTTCTCTC 45

QY 1944 AGGCTGTAGCAAGTTCTGATCTTATACCAACACACAGCAACA 1988
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Db 44 AGGCTGTAGCAAGTNCATGAT-TTATACCCACACACAGCAACA 1

RESULT 2
AL558928
LOCUS 968 bp mRNA linear EST 16-FEB-2001
DEFINITION AL558928 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ007Y107 5
prime, mRNA sequence.
ACCESSION AL558928
VERSION AL558928.1 GI:12903928
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 968
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ007Y107"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 210 a 225 c 300 g 231 t 2 others
ORIGIN

Query Match 47.18; Score 944.2; DB 9; Length 968;
Best Local Similarity 99.2%; Pred. No. 9.9e-236;
Matches 957; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 31 GCTCAGTTTCTTCAGCGGGGCACTGGGAAGCGGCATGCACTGCAGGGCATCTCGGTCG 90
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QY 91 TGGAGCTGTCCGGCTCGGCGGCGGCGGCTTCTGTGCTATGCTCTGCTGACTCGGGG 150
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Db 61 TGGAGCTGTCCGGCTCGGCGGCGGCGGCGGCTTCTGTGCTATGCTCTGCTGACTCGGGG 120

QY 151 CGCGTGTGTACGCGTGAACCGGCGGCGGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 210
|||||
Db 121 CGCGTGTGTACGCGTGAACCGGCGGCGGCGGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 180

QY 211 GCAAGCGCTGCTAGTGTGGAACCTGAAGCAGCGCGGGGAGCGCGGCTGCTGCGGCTC 270
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Db 181 GCAAGCGCTGCTAGTGTGGAACCTGAAGCAGCGCGGGGAGCGCGGCTGCTGCGGCTC 240

Db	QY	271	TGTGCAAGCGGTCGGATGTGCTGCTGGAGCCCTTCCCGCGGGTGTGATGGAGAACTCC	330
		241	TGTGCAAGCGGTCGGATGTGCTGCTGGAGCCCTTCCCGCGGGTGTGATGGAGAACTCC	300
QY	331	AGCTGGGCCAGAGATTTCTGACGGGGAATAATCCAGGCTTATTATGCCAGGCTGAGTG	390	
Db	301	AGCTGGGCCAGAGATTTCTGACGGGGAATAATCCAGGCTTATTATGCCAGGCTGAGTG	360	
QY	391	GATTTGGCCAGTCAGGAAGCTTCTGCCCCGTTAGCTGGCCACGATATCAACTATTTGGCTT	450	
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QY	631	CATATTTAAGTTCTTTTCTGTGTGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	690	
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QY	871	AGAAGTTTGACAGATGTATTTGCAAGAAGACGAGAGGACAGAGTGTGTCAATCTTGCAGC	930	
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QY	931	GCACAGATGCTGTGTGACTCCGCTTCTGACTTTTGAAGAGGTGTTCATCATGATCACA	990	
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QY	991	ACAAG 995		
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	/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT	293 a 186 c 181 g 289 t 10 others
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Best Local Similarity	97.9%; Pred. No. 5.3e-226;
Matches 942; Conservative	6; Mismatches 10; Indels 4; Gaps 3;
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902	AGGGATCCTGTCATAGGAGAACACACTGAGGAGATATTTGAAGAAATTTGGATTCASCCGC 843
1149	GAAGAGATTTTATCAGCTTAACCTCAGATAAATATCATTTGAAGTAAATAGTAAAGCTAGT 1208
842	GAAGAGATTTTATCAGCTTAACCTCAGATAAATATCATTTGAAGTAAATAGTAAAGCTAGT 783
1209	CTCTAATCTCCAGGCCACGCGCTCAAGTGAATTTGAATTTGATTTTACAGTGTAGAGTA 1268
782	CTCTAATCTCCAGGCCACGCGCTCAAGTGAATTTGAAMACTGCATTTACAGTGTAGAGTA 723
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722	ACACATAACATTTGATGCATGGAACATGAGGAACAGTATTACAGTGTCTACCACTCT 663
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1389	ATCATTAGGGCTTTTGTATTTATTAACCTTTGGGTACTTATACATAAATTATGGTACTTAT 1448
602	ATCATTAGGGCTTTTGTATTTATTAACCTTTGGGTACTTATACATAAATTATGGTACTTAT 543
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542	CTGCCCTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTTCTGACTTATATTTGAA 483
1509	TGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACATTTATTTACA 1568
482	TGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATATACATTTATTTACA 423
1569	CTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAAATTTGATGTGATTAAGATC 1628
422	CTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAAATTTGATGTGATTAAGATC 363
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1689	CTAAGCACATTTCCAAACTTTAGCAACAGTTATCACACTTTTGTAATTTGCAAGAAAGATT 1748
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Db 242 TCACCTGTATGAATCAGATGCCCTCACTGAAAAACATATCCAAATAATGAGGAA 183
OY 1809 ATGTGTGGCTCACTACGTAGAGTCCAGAGGACAGTCACTTTAGGGTTGCCTGTATCC 1868
Db 182 ATGTGTGGCTCACTACGTAGAGTCCAGAGGACAGTCACTTTAGGGTTGCCTGTATCC 123
OY 1869 AGTAACCTCGGGGCTGTCTCCCGTGGGTCTCTGGGCTGTACAGCTTCTCTCCATGT 1928
Db 122 AGTAACCTCGGGGCTGTCTCCCGTGGGTCTCTGGGCTGTACAGCTTCTCTCCATGT 63
OY 1929 GTTGTATTTCTCTCAGGCTGTAGC-AACTTCTGGATCTTATACCAACACAGCAAC 1987
Db 62 GTTGTATTTCTCTCAGGCTGTAGCNAAGTTCTGGATCTTATACCAACACAGCAAG 3
OY 1988 AT 1989
Db 2 AT 1

RESULT 4
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LOCUS AL558977 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ008YK07 5
DEFINITION prime, mRNA sequence.
ACCESSION AL558977
VERSION AL558977.1 GI:12904022
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source location/Qualifiers
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/tissue_type="T cells from T cell leukemia"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 180 a 213 c 281 g 209 t 5 others
ORIGIN

Query Match 42.5%; Score 852.2; DB 9; Length 888;
Best Local Similarity 99.2%; Pred. No. 1.1e-211;
Matches 862; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
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Db 20 TTGCAGGCTGCTGGGCTAGGGCTGCTCAGTTCTTCACGGGGGCACTGGGAA 79
OY 61 GCGCCATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCCTGGCCCGCCGCT 120
Db 80 GCGCCATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCCTGGCCCGCCGCT 139

OY 121 TCTGTGCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGACCGCGCGCT 180
Db 140 TCTGTGCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGACCGCGCGCT 199
OY 181 CCCGCTACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGC 240
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Db 260 AGCCGGGGGAGCCCGCGTGTGCGGGCTGTGTCAAGCGGTGATGTGCTGTGAGC 319
OY 301 CCTTCCCGCGGCTGTATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAA 360
Db 320 CCTTCCCGCGGCTGTATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAA 379
OY 361 ATCCAAGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGACTTCTGCCGCT 420
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OY 421 TAGCTGGCCACGATATCAACTATTGGCTTTGTACAGTGTCTCAAAAATTGGCAGAA 480
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Db 500 GTGTGAGAACTCCGTATGCCCCGCTGAATCTCCTGCTGACTTTGCTGCTGCTTA 559
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Db 560 TGTGTGCACTGGGCAATTATATGGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGG 619
OY 601 TCATTGATGCAATATATGTTGGAAGAACACATATTTAAGTCTTTCTGTGAAACCTC 660
Db 620 TCATTGATGCAATATATGTTGGAAGAACACATATTTAAGTCTTTCTGTGAAACCTC 679
OY 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGTGGAGCACCTT 720
Db 680 AGAAATCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGTGGAGCACCTT 739
OY 721 TCTATACGACTTACAGGACAGACAGATGGGGAATTGATGGCTG-TTGGAGCAATAGAACCC 779
Db 740 TCTATACGACTTACAGGACAGACAGATGGGGAATTGATGGCTGTTGGAGCAATARAACC 799
OY 780 CAGTTCTACAGCTGCTGTATCAAAAGACCTTGGACTTAAAGTCTGTATGAACCTTCCCAATCAG 839
Db 800 CAGTTCTACAGCTGCTGTATCAAAAGACCTTGGACTTAAAGTCTGTATGAACCTTCCCAATCAG 859
OY 840 ATGAGCATGATGATTTGGCCAGAAATGAA 868
Db 860 ATGAGCATGATGATTTGGCCAGAAATGAA 888

RESULT 5
BG741165 955 bp mRNA linear EST 15-MAY-2001
LOCUS BG741165 602631843F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',
DEFINITION mRNA sequence.
ACCESSION BG741165 GI:14051818
VERSION BG741165.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.


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QY 183 CGCTACGAGCTGAGCCGCTGGGGCCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCAG 242
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Db 181 CGCTACGAGCTGAGCCGCTGGGGCCGGGCAAGCGCTCGCTAGTGTGCTGACCTGAAGCAG 240
QY 243 CCGCGGGGAGCCCGCTGCTGCGGGCTCTGTGCAAGCGGTGGATGTGCTGCTGAGACCC 302
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Db 241 CCGCGGGGAGCCCGCTGCTGCGGGCTCTGTGCAAGCGGTGGATGTGCTGCTGAGACCC 300
QY 303 TTCGCCCGGGTGTCAAGGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAT 362
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Db 301 TTCGCCCGGGTGTCAAGGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAT 360
QY 363 CCAAGGCTTATTATGCGCAGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTA 422
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Db 601 CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGGAATACTCA 660
QY 662 GAAATCGAGTCTGTGGGAACACCTCGAGGACAGAAATGTTGATGTTGAGCACCTTT 721
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Db 661 GAAATGAGTCTGTGGGAACACCTCGAGGACAGAAATGTTGATGTTGAGCACCTTT 720
QY 722 CTATACGACTTACAGAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 781
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Db 721 CTATACGACTTACAGAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 780
QY 782 GTTCTACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 841
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Db 781 GTTCTACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 840
QY 842 GAGCATGGATGATGGCCAGAAATGAAGAAGAA 874
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Db 841 GAGCATGGATGATGGSCAGAAATGAAGAAGAA 873

RESULT 7
AL571115/c 838 bp mRNA linear EST 16-FEB-2001
DEFINITION AL571115 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1027YJ12 3
prime, mRNA sequence.
ACCESSION AL571115
VERSION AL571115.1 GI:12928089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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            /db_xref="taxon:9606"
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/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 236 a 181 c 152 g 265 t 4 others
ORIGIN

Query Match 41.2%; Score 826.2; DB 9; Length 838;
Best Local Similarity 98.8%; Pred. No. 6.9e-205;
Matches 828; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 726 ACGACTTACAGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCGAGTTC 785
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Db 838 ACAACTAACAGAAACAGMAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCGAGTTC 779
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Db 778 TACGAGCTGCTGATCAAAAGCACTTGGACTAAAKTCTGATGAACCTCCCAATCAGATGAGC 719
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Db 718 ATGATGATTTGCCAGAAATGAAGAAGTTTGCAGATGTATTGCAAGAAGAGCAAG 659
QY 906 GCAGAGTGTGTCAAAATCTTTGACGGGCACAGATGCGCTGTGACTCCGGTCTGACTTTT 965
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Db 658 GCAGAGTGTGTCAAAATCTTTGACGGGCACAGATGCGCTGTGACTCCGGTCTGACTTTT 599
QY 966 GAGGAGGTGTTCATCATGATCACAACAAGGAGGCGCTTTATCACCAGTGAAGAG 1025
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Db 598 GAGGAGGTGTTCATCATGATCACAACAAGGAGGCGCTTTATCACCAGTGAAGAG 539
QY 1026 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAACACCCCAAGCATCCCTCTTTC 1085
    |||||||
Db 538 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAACACCCCAAGCATCCCTCTTTC 479
QY 1086 AAAAGGATCCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTACG 1145
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Db 478 AAAAGGATCCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTACG 419
QY 1146 CGCGAAGAGATTTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGCT 1205
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Db 418 CGCGAAGAGATTTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGCT 359
QY 1206 AGTCTCTAACTTCCAGCGCCAGCGCTCAAGTGAATTTGAATCTGCATTTACAGTGA 1265
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Db 358 AGTCTCTAACTTCCAGCGCCAGCGCTCAAGTGAATTTGAATCTGCATTTACAGTGA 299
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QY 1326 TCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAATAATG 1385
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Db 238 TCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAATAATG 179
QY 1386 GTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATGTTAGT 1445
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Db 178 GTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATGTTAGT 119
QY 1446 ATTCTGCTTCCAGTTTGGCTGATATATTGTTGATATTAAAGATTCTGACTTAATTTT 1505
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Db 118 ATTCTGCTTCCAGTTTGGCTGATATATTGTTGATATTAAAGATTCTTACTTAATTTT 59
QY 1506 GATGGGTTCTAGTGAAGAAAGAAATGATATATTCTTGAAGACATCGATATACATTTAT 1563
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Db 58 GAATGGCTCTAGTGAAGAAGATGATATATTCTTGAGACATCGATATACATTNAT 1
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RESULT 8
AL551698
LOCUS 842 bp mRNA linear EST 16-FEB-2001
DEFINITION AL551698 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI062YP05 5
prime, mRNA sequence.
ACCESSION AL551698
VERSION AL551698.1 GI:12889898
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 842)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI062YP05"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 189 a 197 c 247 g 198 t 11 others
ORIGIN
Query Match 40.7%; Score 815.8; DB 9; Length 842;
-Best Local Similarity 97.9%; Pred.No.3.6e-202;
Matches 825; Conservative 9; Mismatches 8; Indels 1; Gaps 1;
QY 63 GCCATGGCAGTGCAGGGCATCTCGTGTGAGAGCTGTCCGGCCCTGGCCCCGGCCGCTTC 122
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Db 1 GCCATGGCAGTGCAGGGCATCTCGTGTGAGAGCTGTCCGGCCCTGGCCCCGGCCGCTTC 60
QY 123 TGTGCTATGCTCTGGCTGACTTGGGGCGCGTGTGTACGCGGTGACCCGCGCTCC 182
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Db 61 TGTGCTATGCTCTGGCTGACTTGGGGCGCGTGTGTACGCGGTGACCCGCGCTCC 120
QY 183 CGCTACGACGTGAGCCGCTGTGGCGCGGGGGAAGCGCTCGCTAGTGTGAGCTGAAGCAG 242
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Db 121 CGCTACGACGTGAGCCGCTGTGGCGCGGGGGAAGCGCTCGCTAGTGTGAGCTGAAGCAG 180
QY 243 CCGCGGGGAGCCCGCGCTGCTGCGCGCGCTGTGTGCAAGCGGTGCGTGTGAGCCCC 302
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Db 181 CCGCGGGGAGCCCGCGTGTGCGCGCGCTGTGTACAAAGCSGTCSGATGTGCTGTGAGCCC 240
QY 303 TTCGCGCGCGGTGTATGAGAAACTCCAGCTGGGCCCAAGAGATTCTGACAGCGGAAAT 362
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Db 241 TTCGCGCGCGGTGTATGAGAAACTCCAGCTGGGCCCAAGAGATTCTGACAGCGGAAAT 300
QY 363 CCAAGGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTTCGCCGTTA 422
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Db 301 CCAAGGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTTCGCCGTTA 360
QY 423 GCTGGCCAGCATATCAACTATTGGCTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGT 482

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Db 361 GCTGGCCAGCATATCAACTATTGGCTTTTCTKTCAGGTTCTCTCAAAAATTGGCAGAGT 420
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QY 483 GGTGAGATCCGATATGCCCGCTGAATCTCCTGCGTACTTTGCTGTGTGCGCTTATG 542
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Db 421 GGTGAATAATCCSTATSCCCSCTGAATCTCCTGCGTACTTTGCTGTGTGCGCTTATG 480
QY 543 TGTGACATGGGCATTATTAATGGCTTTTGTGACCGCACAGCAGTGGCAAGGTCAAGTTC 602
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Db 481 TGTGACATGGGCATTATTAATGGCTTTTGTGACCGCACAGCAGTGGCAAGGTCAAGTTC 540
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QY 723 TATACGACTTACAGAGACAGATGGGGAATTCATGCTGTGAGCAATAGAACCCAG 782
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Db 661 TATACGACTTACAGAGACAGATGGGGAATTCATGCTGTGAGCAATAGAACCCAG 720
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Db 721 TTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATG 780
QY 843 AGCATGATGATTTGGCCGAAATGAAGAGAGAGTTTGCAGATGATTTGCCAAGAGACG 902
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Db 781 AGCATGATGATTTGGCCGAAATGAAGAGAGAG-TTTGCAGATGATTTGCCAAGAGAGM 839
QY 903 AAG 905
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Db 840 AAG 842

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RESULT 9
 LOCUS BM723657 823 bp mRNA linear EST 01-MAR-2002
 DEFINITION UI-E-EJ0-a1q-n-09-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
 UI-E-EJ0-a1q-n-09-0-UI 5', mRNA sequence.
 ACCESSION BM723657
 VERSION BM723657.1 GI:19044988
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 823)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250.
 Fax: 319 335 9565
 Email: msouares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seg primer: M13 Reverse
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 source
 1. 823
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ0-a1q-n-09-0-UI"

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/clone_lib="UI-E-EJ0"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCCAT;
optic nerve, CCATTAGTG; retina, CCGCG; Retina foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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BASE COUNT 249 a 156 c 191 g 224 t 3 others

ORIGIN

Query Match 40.6%; Score 813.6; DB 14; Length 823;
Best Local Similarity 99.18; Pred. No. 1.4e-201;
Matches 816; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 CAGAAATCGAGTCTGTGGAGCACCTCGAGAGACAGATGTTGGATGGTGAGCACCCT 60

OY 720 TTCTATACGACTTACAGACAGATGGGAATTCATGGCTGTTGGACAATAGAACCC 779
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Db 61 TTCTATACGACTTACAGACAGATGGGAATTCATGGCTGTTGGACAATAGAACCC 120

OY 780 CAGTCTACGAGCTGCTCAAAAGGAGCTTGAGCTAAAGTCTGATGAACCTCCCAATCAG 839
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Db 121 CAGTCTACGAGCTGCTCAAAAGGAGCTTGAGCTAAAGTCTGATGAACCTCCCAATCAG 180

OY 840 ATGAGCATGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTGCCAAGAACG 899
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Db 181 ATGAGCATGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTGCCAAGAACG 240

OY 900 ACGAAGGCAGAGTGGTGTCAAAATCTTTGACGGGCACAGATGCCCTGTGACTCCGGTCTG 959
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Db 241 ACGAAGGCAGAGTGGTGTCAAAATCTTTGACGGGCACAGATGCCCTGTGACTCCGGTCTG 300

OY 960 ACTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAGGCGCTCGTTATCACCAGT 1019
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OY 1020 GAGGAGCAGAGCTGAGCCCCCCCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCT 1079
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Db 361 GAGGAGCAGAGCTGAGCCCCCCCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCT 420

OY 1080 TCTTTCAAAAGGATCCCTTTCATAGGAGAACACACATGAGAGATACTTGAAGATTGGA 1139
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Db 421 TCTTTCAAAAGGATCCCTTTCATAGGAGAACACACATGAGAGATACTTGAAGATTGGA 480

OY 1140 TTCAGCCCGGAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAGGTA 1199
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Db 481 TTCAGCCCGGAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAGGTA 540

OY 1200 AAAGCTAGTCTTAACCTCCAGGCCCTCAAGTGAATTTGAATACCTGCATTACAG 1259
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Db 541 AAAGCTAGTCTTAACCTCCAGGCCCTCAAGTGAATTTGAATACCTGCATTACAG 600

OY 1260 TGTAGAGTAACACATATGTTATGATGAGAAACATGAGGAACAGTATTACAGTGTCC 1319
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OY 1380 AAAATGCTTATCATTTAGCGCTTTTGATTTATATAAACTTTGGGTACTTATCTAAATTATG 1439
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Db 721 AAAATGCTTATCATTTAGCGCTTTTGATTTATATAAACTTTGGGTACTTATCTAAATTATG 780

OY 1440 GTAGTTATTTCTGCGCTTCCAGTTTGCTTGATATATTGTTGATA 1482
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Db 781 GTAGTTATTTCTGCGCTTCCAGTTTGCTTGATATATTGTTGATA 823

RESULT 10
AK002401
LOCUS
DEFINITION
Mus musculus adult male kidney cDNA, RIKEN full-length enriched
library, clone:0610009H21:alpha-methylacyl-CoA racemase, full
insert sequence.
ACCESSION
AK002401
VERSION
AK002401.1 GI:12832356
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA,
clone:0610009H21.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Carninci,P. and Hayashizaki,Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636

REFERENCE
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861

REFERENCE
AUTHORS
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaide,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staudli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Sakamoto,N., Sasaki,H.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seta,T., Shibata,Y., Storch,K.F., Suzuki,H.,
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Db	857	AAGCGAAGATGGTGCCAGATCTTTGACGGGACAGATGCGTGTGTGACCCCAAGTGTGACG	916
OY	963	TTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGCTCGTTATCACCAGTGAG	1022
Db	917	TTTGAGGAGGCCCTCCACCACCAACACAAGAAAGGCGCTCCCTTCATCAGTATGAG	976
OY	1023	GAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTCT	1082
Db	977	GAGCAGCTCCCGAGCCCCCGCCCTGCACCTCTGCTTCCAGAACTCCTGCCGTCCATCT	1036
OY	1083	TTCAAAAGGATCCCTTTCATAGAGAACACACACTGAGGAGATCTTGAAGATTGGATTTC	1142
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OY	1143	AGCGCCGAAGAGATTATTCAGCTTAACTCAGATAAATCATTTGAAAGTAATAGGTAATA	1202
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OY	1263	AGAGTAACACATTAACATTTGTATGCATGGAACATGAGGAACAGATATTACAGT - GTCCCTA	1321
Db	1215	GGAGGGATGCCACACAATTTGTGTATGGAATATGTGATGAACAGCAATGAAGTCATCCAA	1274
OY	1322	CCACTCTAATCAAGAAAAAAGATTAACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA	1381
Db	1275	ATATCCCAATCAGATCCCAAGCAAGAGCTGGTTACAGGATTAACGATTCGCCCCCTTACGCT	1334
OY	1382	AATGTTATCATTTAGGGCTTTTGATTTTATAAACTTTGGGTACTTTACTAAATTATGGT	1441
Db	1335	GCTTATCAGAGCCCTCTGATTTGAGGAAAAATTTGTGTGTGTACTGATGAATTAATCTTGTGGC	1394
OY	1442	AGTTATTTCTGCCCTTCCAGTTTGTGTTGATATATTGTTGATATTAAGATTCTTGACTTATA	1501
Db	1395	AGCT-TTCTGCCCTTTCAGTTCCCTTGGTGAAGTGTATCCATTTAATTAACCCCTTTTATA	1453
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Db	1454	AATACAA 1460	

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RESULT 11
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LOCUS
DEFINITION AL545355 824 bp mRNA linear EST 16-FEB-2001
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prime, mRNA sequence.
ACCESSION AL545355
VERSION AL545355.1 GI:12877836
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 824)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Source 1..824

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/clone="CSODI027YJ12"
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
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enriched, double-stranded cDNA was digested with Not I and

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cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>

Query Match	39.78;	Score 796.4;	DB 9;	Length 824;
Best Local Similarity	99.28;	Pred. No. 4.3e-197;		
Matches 819; Conservative	2;	Mismatches 3;	Indels 2;	Gaps 2;

QY	71	ACTGCAGGGCATCTCGGTCGTGAGCTGTCCGGCCCTGGCCCCGGGGCCGTTCTGTGCTAT	130
Db	1	ACTGCAGGGCATCTCGGTCGTGAGCTGTCCGGCCCTGGCCCCGGGGCCGTTCTGTGCTAT	60
QY	131	GGTCTGCGCTGACTTCCGGGCGCGCTGTGTACCGCTGGACC GGCCCGCGCTCCCGCTACGA	190
Db	61	GGTCTGCGCTGACTTCCGGGCGCGCTGTGTACCGCTGGACC GGCCCGCGCTCCCGCTACGA	120
QY	191	CGTAGCCGCTTGGGCCGGGCAAGCGCTCCGCTAGTGTCTGGACCTGAAGCAGCCGCGGGG	250
Db	121	CGTAGCCGCTTGGGCCGGGCAAGCGCTCCGCTAGTGTCTGGACCTGAAGCAGCCGCGGGG	180
QY	251	AGCCGCGCTGCTGCGGCGTCTGTGCAAGCGCTCCGATGTGCTGTGAGGCCCTTCCGCCG	310
Db	181	AGCCGCGCTGCTGCGGCGTCTGTGCAAGCGCTCCGATGTGCTGTGAGGCCCTTCCGCCG	240
QY	311	CGGTGTATGAGAAACTCCAGCTGGGCCACAGATTTCTGCAGCGGGAAATCCAAGGCT	370
Db	241	CGGTGTATGAGAAACTCCAGCTGGGCCACAGATTTCTGCAGCGGGAAATCCAAGGCT	300
QY	371	TATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCA	430
Db	301	TATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCA	360
QY	431	CGATATCAACTATTTTGGCTTTGTACAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGAGAA	490
Db	361	CGATATCAACTATTTTGGCTTTGTACAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGAGAA	420
QY	491	TCCGTATCCCCCGCTGAATCTCTGGCTGACTTTGCTGTGGTGGCCTTATGTGCACT	550
Db	421	TCCGTATCCCCCGCTGAATCTCTGGCTGACTTTGCTGTGGTGGCCTTATGTGCACT	480
QY	551	GGGCATTATATGGCTCTTTTGCACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGC	610
Db	481	GGGCATTATATGGCTCTTTTGCACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGC	540
QY	611	AAATATGGTGAAGGAACAGCATATTTAAAGTTCTTTCTGTGAAAACCTCAGAAATCGAG	670
Db	541	AAATATGGTGAAGGAACAGCATATTTAAAGTTCTTTCTGTGAAAACCTCAGAAATTGAG	600
QY	671	TCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTCTATACGAC	730
Db	601	TCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGGTGGAGCA - CTTCTATACGAC	659
QY	731	TTACAGGACAGCAGATGGGAATTCAATGCGCTGTGGACAATAGAACCCCAAGTTCTACGA	790
Db	660	TTACAGGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAA - CCCAGTTCTACGA	718
QY	791	GCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGA	850
Db	719	GCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGA	778
QY	851	TGATTGGCCAGAAATGAAGAAGAGTTGCAAGATGATTGGCAAAG	896
Db	779	TGATTGGCCAGAAATGAAGAAGAGTTTTCAGATGTATTTTCAGAG	824

RESULT 12
BQ962523


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LOCUS      BQ962523      890 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT_8817570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6379327
5', mRNA sequence.
ACCESSION  BQ962523
VERSION    BQ962523.1  GI:22378001
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 890)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            plate: L1CM2566 row: c column: 08
            High quality sequence stop: 750.
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                /clone_lib="NIH_MGC_42"
                /tissue_type="epithelioid carcinoma cell line"
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                Site_2: EcoRI; cDNA made by oligo-dT priming.
                directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
BASE COUNT 187 a 221 c 278 g 203 t 1 others
ORIGIN
Query Match 39.0%; Score 781.8; DB 14; Length 890;
Best Local Similarity 99.1%; Pred. No. 2.9e-193;
Matches 786; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 24 AAGGGCTGCTACGTTTCTTCACGGGGGACACTGGGAAGCGCCATGGCACTGCAGGGCATC 83
DB 1 AAGGGCTGCTACGTTTCTTCACGGGGGACACTGGGAAGCGCCATGGCACTGCAGGGCATC 60
QY 84 TCGGTCGTGAGCTGTCCGGCTGGCCCCCGGGCCGTTCTGTGCTATGGTCTCGGCTGAC 143
DB 61 TCGGTCATGAGCTGTCCGGCTGGCCCCCGGGCCGTTCTGTGCTATGGTCTCGGCTGAC 120
QY 144 TTCGGGGCGCGTGTGTACGGCGTGAACCGGCGCGCTCCCGCTACGACGTGAGCCGCTTG 203
DB 121 TTCGGGGCGCGTGTGTGTACGGCGTGAACCGGCGCGCTCCCGCTACGACGTGAGCCGCTTG 180
QY 204 GGGCGGGGCAAGCGCTCGTAGTCTTGACCTGAAGCAGCCGCGGGAAGCCGCGCTGCTG 263
DB 181 GGGCGGGGCAAGCGCTCGTAGTCTTGACCTGAAGCAGCCGCGGGAAGCCGCGCTGCTG 240
QY 264 CGGCGTCTGTGCAAGCGGTGATGTGCTGTGAGCCCTTCCGCGCGGTGTATGAG 323
DB 241 CGGCGTCTGTGCAAGCGGTGATGTGCTGTGAGCCCTTCCGCGCGGTGTATGAG 300
QY 324 AACTTCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAGAGCTTATTATGCCAGG 383
DB 301 AACTTCAGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAGAGCTTATTATGCCAGG 360

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QY 384 CTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCACTAT 443
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QY 444 TTGGCTTTGTACAGTGTCTCTCAAAAATTGGCAGAAAGTGGTAATCCGTATGCCCG 503
DB 421 TTGGCTTTGTACAGTGTCTCTCAAAAATTGGCAGAAAGTGGTAATCCGTATGCCCG 480
QY 504 CTGAATCTCTCGGCTGACCTTGTGCTGTGTGGCCCTTATGTGTGCACTGGGCATTTAATG 563
DB 481 CTGAATCTCTCGGCTGACCTTGTGCTGTGTGGCCCTTATGTGTGCACTGGGCATTTAATG 540
QY 564 GCTCTTTTGTACCCGACACGACACGACATGGCAAGGTCAGTCAATGATGCAATATGGTGAA 623
DB 541 GCTCTTTTGTACCCGACACGACACGACATGGCAAGGTCAGTCAATGATGCAATATGGTGAA 600
QY 624 GGAACAGCATATTTAAGTTCTTTCTGTGGA AAAACTCAGAAATCGAGTCTGTGGAGCA 683
DB 601 GGAACAGCATATTTAAGTTCTTTCTGTGGA AAAACTCAGAAATCGAGTCTGTGGAGCA 660
QY 684 CCTGAGGACAGAACATGTTGGATGTGAGACACCTTTCTATACGACTTACAGGACAGCA 743
DB 661 CCTGAGGACAGAACATGTTGGATGTGAGACACCTTTCTATACGACTTACAGGACAGCA 720
QY 744 GATGGGAATTTCATGCTGTGTGAGCAATAGAACCCAGTCTTACAGCTGCTGATCAAA 803
DB 721 GATGGGAATTTCATGCTGTGTGAGCAATAGAACCCAGTCTTACAGCTGCTGATCAAA 780
QY 804 GGACTTGGACTAA 816
DB 781 GGTTGGGAGAA 793

RESULT 13
LOCUS      BQ941482      890 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT_8821476 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6203684 5', mRNA sequence.
ACCESSION  BQ941482
VERSION    BQ941482.1  GI:22356960
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 890)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            plate: L1AM13623 row: 1 column: 21
            High quality sequence stop: 621.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:6203684"
                /clone_lib="Lupski_sciatic_nerve"
                /sex="male"
                /tissue_type="sciatic nerve"
                /dev_stage="adult, 70 yr"
                /lab_host="DH10B"
                /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
                NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:

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5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 253 a 189 c 219 g 223 t 6 others
ORIGIN

Query Match 36.3%; Score 728; DB 14; Length 890;
Best Local Similarity 99.2%; Pred. No. 3.4e-179;
Matches 731; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 461 TCCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGA 520
Db 1 TCCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATCTCTGGCTGA 60
QY 521 CTTTGCTGCTGGTGGCCCTTATGCTGCACTGGGCATTTATATGGCTCTTTTGACCGCAC 580
Db 61 CTTTGCTGCTGGTGGCCCTTATGCTGCACTGGGCATTTATATGGCTCTTTTGACCGCAC 120
QY 581 ACGCACTGGCAAGGTCAGGTCATTTGATGCAATATATGTTGAAGAACATATTTAAG 640
Db 121 ACGCACTGGCAAGGTCAGGTCATTTGATGCAATATATGTTGAAGAACATATTTAAG 180
QY 641 TTCTTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACAT 700
Db 181 TTCTTTTCTGTGGAATACTCAGAAATTTGAGTCTGTGGGAAGCACCTCGAGGACAGAACAT 240
QY 701 GTTGATGGTGGAGCACCTTTCTATACGACTTACAGAGACAGATGGGAATTCATGGC 760
Db 241 GTTGATGGTGGAGCACCTTTCTATACGACTTACAGAGACAGATGGGAATTCATGGC 300
QY 761 TGTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAGGACTTGACTAAAGTC 820
Db 301 TGTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAGGACTTGACTAAAGTC 360
QY 821 TGAAGAATCTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGAAGATTGTC 880
Db 361 TGAAGAATCTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGAAGATTGTC 420
QY 881 AGATGTATTTGCAAGAAGACGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGC 940
Db 421 AGATGTATTTGCAAGAAGACGAGAGTGGTGTCAAAATCTTTGACGGCACAGATGC 480
QY 941 CTGTGTGACTCCGGTCTGACTTTTGAGGAGGTGTTCATCATGATCACAACAAGGAACG 1000
Db 481 CTGTGTGACTCCGGTCTGACTTTTGAGGAGGTGTTCATCATGATCACAACAAGGAACG 540
QY 1001 GGGCTGCTTTATCACCAGTGAAGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGT 1060
Db 541 GGGCTGCTTTATCACCAGTGAAGAGCAGGACGTGAGCCCGCCCTGCACCTCTGCTGT 600
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Db 601 AAACACCCCGACCATCCCTTCTTCAAAAAGGATCCTTCATAGGAGAACAACATGAGA 660
QY 1121 GATFACTTGAAGATTTGATTCAGCCCGGAGAGATTTATCAGCTTAAGTCAAGTAAAT 1180
Db 661 GATFACTTGAAGATTTGATTCAGCCCGGAGAGATTTATCAGCTTAAGTCAAGTAAAT 720
QY 1181 CATTGAAGTAAATAGG 1197
Db 721 CATTGAAGTAAATAGG 737

RESULT 14
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DEFINITION 602975075F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114130 5',
mRNA sequence.
ACCESSION BI256255

VERSION BI256255.1 GI:14810488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1127 row: f column: 19
High quality sequence stop: 751.

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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 174 a 189 c 253 g 192 t
ORIGIN

Query Match 35.9%; Score 720.6; DB 13; Length 808;
Best Local Similarity 98.1%; Pred. No. 2.9e-177;
Matches 792; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

QY 93 GAGCTGTCCGGCTGGCCCGGGCCCGCTTCTGTGCTATGCTCCTGGCTGACTTCGGGGCG 152
Db 1 GAGCTGTCCGGCTGGCCCGGGCCCGCTTCTGTGCTATGCTCCTGGCTGACTTCGGGGCG 60
QY 153 CGTGTGTACGCGGTGAGACCGCGCGGCTCCCGCTACGACGTGAGCCGCTGGCGGGGGC 212
Db 61 CGTGTGTACGCGGTGAGACCGCGCGGCTCCCGCTACGACGTGAGCCGCTGGCGGGGGC 120
QY 213 AAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGGGGAGCCCGGTGCTGCGGCTCTG 272
Db 121 AAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGGGGAGCCCGGTGCTGCGGCTCTG 180
QY 273 TGCAGCGGTGCGATGTGCTGTGAGACCCCTTCGCCCGCGGTGTCATGAGAAACTCCAG 332
Db 181 TGCAGCGGTGCGATGTGCTGTGAGACCCCTTCGCCCGCGGTGTCATGAGAAACTCCAG 240
QY 333 CTGGGCCCGAGAGATTCGACGCGGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTGA 392
Db 241 CTGGGCCCGAGAGATTCGACGCGGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTGA 300
QY 393 TTTGGCCAGTCAAGAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 452
Db 301 TTTGGCCAGTCAAGAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 360
QY 453 TCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGATATGCCCGCTGAATCTC 512
Db 361 TCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGATATGCCCGCTGAATCTC 420
QY 513 CTGGCTGACTTTGCTGTGTGCTGGCCCTTATATGTGCTGAGGCAATATATATGCTCTTTT 572
Db 421 CTGGCTGACTTTGCTGTGTGCTGGCCCTTATATGTGCTGAGGCAATATATATGCTCTTTT 480
QY 573 GACCGCACACGACACTGGCAAGGGTCAGGTCATGTGCAAAATATATGTTGAAGAACACAGCA 632


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QY 301 CCTCCGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAA 360
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Db 301 CCTCCGCCGGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAA 360
QY 361 ATCCAAGGCTTATTATGCGCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGT 420
    |||
Db 361 ATCCAAGGCTTATTATGCGCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGT 420
QY 421 TAGCTGGCCAGATATCAACTATTGGCTTTGTCAGGTGTTCTCAAAAATTGGCAGAA 480
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Db 421 TAGCTGGCCAGATATCAACTATTGGCTTTGTCAGGTGTTCTCAAAAATTGGCAGAA 480
QY 481 GTGTGAGAAATCCGTATGCCCCGCTGAATCTCCGTGACTTTGCTGCTGCTGCTTA 540
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Db 481 GTGTGAGAAATCCGTATGCCCCGCTGAATCTCCGTGACTTTGCTGCTGCTGCTTA 540
QY 541 TGTGTGACTGGGCATTATATGGCTTTTGGACCGCACAGCACTGGCAAGGTCAGG 600
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Db 541 TGTGTGACTGGGCATTATATGGCTTTTGGACCGCACAGCACTGGCAAGGTCAGG 600
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Db 601 TCATTGATCAAAATATGTTGGAAGAACAGCATATTAAAGTTCTTTCTGTGAAAACTC 660
QY 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGGTGAGCACCTT 720
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Db 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGGTGAGCACCTT 720
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QY 781 AGTTCTACGAGCTGCTGATCAAAAGGACTGGAATAAGTCTGATGAATCTCCCAATCAGA 840
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Db 841 TGAGCATGATGATTGGCCAGAAATGAGAAGATTGTCAGATGATTTGCAAGAAGA 900
QY 901 CGAAGCAGAGTGTGTCAAATCTTTCAGCGGCACAGATGCTGTGACTCCGGTCTGA 960
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Db 901 CGAAGCAGAGTGTGTCAAATCTTTCAGCGGCACAGATGCTGTGACTCCGGTCTGA 960
QY 961 CTTTGAAGAGTGTGTCATCATGATCAACAACAAGGAGGGCTTTATCACCAGTG 1020
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Db 961 CTTTGAAGAGTGTGTCATCATGATCAACAACAAGGAGGGCTTTATCACCAGTG 1020
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QY 1081 CTTTCAAAAGGGATCCTTTCATAGGAAACACACTGAGGAGATCTGAAGAATTGGAT 1140
    |||
Db 1081 CTTTCAAAAGGGATCCTTTCATAGGAAACACACTGAGGAGATCTGAAGAATTGGAT 1140
QY 1141 TCAGCCGCGAAGAGATTATCAGTTAACTCAGATAAATCATTTGAAGTAA 1200
    |||
Db 1141 TCAGCCGCGAAGAGATTATCAGTTAACTCAGATAAATCATTTGAAGTAA 1200
QY 1201 AAGCTAGTCTTAATCTCCAGGCCCCAGGCTCAAGTGAATTTGAATCTGATTTACAGT 1260
    |||
Db 1201 AAGCTAGTCTTAATCTCCAGGCCCCAGGCTCAAGTGAATTTGAATCTGATTTACAGT 1260
QY 1261 GTAGAGTAACACATATGATGATGGAACATGGAGGAACAGTATTACAGTGTCT 1320
    |||
Db 1261 GTAGAGTAACACATATGATGATGGAACATGGAGGAACAGTATTACAGTGTCT 1320
QY 1321 ACCACTTAATCAAGAAAAAGAAATACAGACTCTGATTTCTACAGTATGATTTCTAA 1380
    |||
Db 1321 ACCACTTAATCAAGAAAAAGAAATACAGACTCTGATTTCTACAGTATGATTTCTAA 1380
QY 1381 AAATGTTATCATTAGGGCTTTGATTTATAAACTTTGGGTACTTATAAATTATGG 1440
```

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Db 1381 AAATGTTATCATTAGGGCTTTGATTTATAAACTTTGGGTACTTATAAATTATGG 1440
QY 1441 TAGTTATTCGCCCTTCCAGTTTGTGCTGATATTTGTTGATATTAAGATCTTGACTTAT 1500
    |||
Db 1441 TAGTTATTCGCCCTTCCAGTTTGTGCTGATATTTGTTGATATTAAGATCTTGACTTAT 1500
QY 1501 ATTTTGAATGGGTCTAGTGAANAAGAAATGATATATCTTGAAGACATCGATATACATT 1560
    |||
Db 1501 ATTTTGAATGGGTCTAGTGAANAAGAAATGATATATCTTGAAGACATCGATATACATT 1560
QY 1561 TATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAATTTGATGTTGA 1620
    |||
Db 1561 TATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAATTTGATGTTGA 1620
QY 1621 TAAAAGTACGTGAACAGAGTGAATGTTGTCATCCAGGCCCTTTGCTTGTGTTGATG 1680
    |||
Db 1621 TAAAAGTACGTGAACAGAGTGAATGTTGTCATCCAGGCCCTTTGCTTGTGTTGATG 1680
QY 1681 ATCTCCCTTAAGCACATTCCAAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1740
    |||
Db 1681 ATCTCCCTTAAGCACATTCCAAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1740
QY 1741 GAAAAGTTTCACTGTATTGAATCAGAAATGCTTCAACTGAAAAAACATATCCAAATA 1800
    |||
Db 1741 GAAAAGTTTCACTGTATTGAATCAGAAATGCTTCAACTGAAAAAACATATCCAAATA 1800
QY 1801 ATGAGAAATGTGTTGGCTCAGTACAGTCCAGAGGACAGTCACTTTAGGTTGC 1860
    |||
Db 1801 ATGAGAAATGTGTTGGCTCAGTACAGTCCAGAGGACAGTCACTTTAGGTTGC 1860
QY 1861 CTGTATCCAGTAATCGGGGCTGTTCCCGTGGGTCTCTGGGCTGCAGCTTCCCTT 1920
    |||
Db 1861 CTGTATCCAGTAATCGGGGCTGTTCCCGTGGGTCTCTGGGCTGCAGCTTCCCTT 1920
QY 1921 CTCCATGTGTTGATTTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCAACACACA 1980
    |||
Db 1921 CTCCATGTGTTGATTTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCAACACACA 1980
QY 1981 CAGCAACATCCAGAAATAAGTTCT 2005
    |||
Db 1981 CAGCAACATCCAGAAATAAGATCT 2005
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RESULT 2
US-10-210-120-104
: Sequence 104, Application US/10210120
: GENERAL INFORMATION:
: APPLICANT: Chinaiyan, Arul M.
: APPLICANT: Rubin, Mark A.
: APPLICANT: Sreekumar, Arun.
: TITLE OF INVENTION: Expression Profile of Prostate Cancer
: FILE REFERENCE: UM-07221
: CURRENT APPLICATION NUMBER: US/10/210,120
: CURRENT FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: US 60/309,581
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: US 60/334,468
: PRIOR FILING DATE: 2001-11-15
: NUMBER OF SEQ ID NOS: 123
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 104
: LENGTH: 2005
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-210-120-104
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Query Match          99.9%; Score 2003.4; DB 8; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 TTGACGCTGCTGGGCTGAGGCTGCTCAGTTTCTTCAGCGGGGCACTGGGAA 60
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Db 1 TTGCAGGCTGCTGGGCTGGGGCTAAGGCTGCTCAGTTTCTTCAGCGGGGCACATGGGA 60
QY 61 GCGCCATGGCAGCTGCAGGGGCAATCGGTGCTGAGCTGTCCGGCTGGCCCCGGGCGGT 120
Db 61 GCGCCATGGCAGCTGCAGGGGCAATCGGTGCTGAGCTGTCCGGCTGGCCCCGGGCGGT 120
QY 121 TCTGTGCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTTACCGGTGGACCGGGCGGCT 180
Db 121 TCTGTGCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTTACCGGTGGACCGGGCGGCT 180
QY 181 CCCGCTAGCAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGC 240
Db 181 CCCGCTAGCAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGC 240
QY 241 AGCCCGGGGAGCCCGCGTGTGCGGGCGTGTGCAAGCGGTGCGATGTGCTGTGAGC 300
Db 241 AGCCCGGGGAGCCCGCGTGTGCGGGCGTGTGCAAGCGGTGCGATGTGCTGTGAGC 300
QY 301 CCTCCCGCGGGTGTATGAGAGAACTCCAGCTGGGGCCAGAGATTCAGACGGGAAA 360
Db 301 CCTCCCGCGGGTGTATGAGAGAACTCCAGCTGGGGCCAGAGATTCAGACGGGAAA 360
QY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCCGGT 420
Db 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCCGGT 420
QY 421 TAGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAA 480
Db 421 TAGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAA 480
QY 481 GTGCTGAGAAATCCGTATGCCCGCTGAATCTCCGTGACTTGTGCTGTGGTGGCTTA 540
Db 481 GTGCTGAGAAATCCGTATGCCCGCTGAATCTCCGTGACTTGTGCTGTGGTGGCTTA 540
QY 541 TGTGTGCACTGGGCATTATATAGGCTCTTTTGACCCGCACACCGCACTGGCAAGGTCAGG 600
Db 541 TGTGTGCACTGGGCATTATATAGGCTCTTTTGACCCGCACACCGCACTGGCAAGGTCAGG 600
QY 601 TCATTGATGCAAAATATGTTGGGAAGCAACAGCATATTTAAAGTCTTTCTGTGAAAACCTC 660
Db 601 TCATTGATGCAAAATATGTTGGGAAGCAACAGCATATTTAAAGTCTTTCTGTGAAAACCTC 660
QY 661 AGAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTGTGATGGTGGAGCACCTT 720
Db 661 AGAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTGTGATGGTGGAGCACCTT 720
QY 721 TCTATACGACTTACAGGACAGAGATGGGAATTCATGCTGTGTGAGCAATAGAACCCC 780
Db 721 TCTATACGACTTACAGGACAGAGATGGGAATTCATGCTGTGTGAGCAATAGAACCCC 780
QY 781 AGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGA 840
Db 781 AGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGA 840
QY 841 TGAGCATGATGATTTGGCCAGAAATGAGAAGATTTCAGATGTATTTGCAAGAAGA 900
Db 841 TGAGCATGATGATTTGGCCAGAAATGAGAAGATTTCAGATGTATTTGCAAGAAGA 900
QY 901 CGAAGGACAGTGTGTCAAAATCTTTGACGGGACAGATGCCCTGTGTGACTCCGGTTCYGA 960
Db 901 CGAAGGACAGTGTGTCAAAATCTTTGACGGGACAGATGCCCTGTGTGACTCCGGTTCYGA 960
QY 961 CTTTGTAGAGGTTGTTCATCATGATCACAACAAGGAACGGGCTGTTATCACCAAGTG 1020
Db 961 CTTTGTAGAGGTTGTTCATCATGATCACAACAAGGAACGGGCTGTTATCACCAAGTG 1020
QY 1021 AGGAGCAGAGCTGAGCCCCCGGCTGACCTGTGCTGTTAAACACCCAGCAATCCCTT 1080
Db 1021 AGGAGCAGAGCTGAGCCCCCGGCTGACCTGTGCTGTTAAACACCCAGCAATCCCTT 1080
QY 1081 CTTTCAAAAGGATCCTTTCATAGGAGAACACACTGAGAGATTTGGAATTTGGAT 1140
Db 1081 CTTTCAAAAGGATCCTTTCATAGGAGAACACACTGAGAGATTTGGAATTTGGAT 1140

QY 1141 TCAGCCGGGAGAGATTTATCAGCTTAACTCAGATTAATCATTTGAAGTAATAGCTAA 1200
Db 1141 TCAGCCGGGAGAGATTTATCAGCTTAACTCAGATTAATCATTTGAAGTAATAGCTAA 1200
QY 1201 AAGCTAGTCTCTAAGTCTCCAGGCGCCGCTCAAGTGAATTTGAATCTGCATTTACAGT 1260
Db 1201 AAGCTAGTCTCTAAGTCTCCAGGCGCCGCTCAAGTGAATTTGAATCTGCATTTACAGT 1260
QY 1261 GTAGAGTAACACATTAACATTTGTATGCAATGGAACATGAGGAACAGATTTACAGTGTCT 1320
Db 1261 GTAGAGTAACACATTAACATTTGTATGCAATGGAACATGAGGAACAGATTTACAGTGTCT 1320
QY 1321 ACCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATCTAA 1380
Db 1321 ACCACTCTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATCTAA 1380
QY 1381 AAATGGTTATCATTAAGGCTTTTGAATTTATAAAACCTTGGTACTTATACTAAATATGG 1440
Db 1381 AAATGGTTATCATTAAGGCTTTTGAATTTATAAAACCTTGGTACTTATACTAAATATGG 1440
QY 1441 TAGTTATTTCTGCTTCCAGTGTGCTTGATATATTTGTTGATATTTAAGATTTCTGACTTAT 1500
Db 1441 TAGTTATTTCTGCTTCCAGTGTGCTTGATATATTTGTTGATATTTAAGATTTCTGACTTAT 1500
QY 1501 ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATT 1560
Db 1501 ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATT 1560
QY 1561 TATTTACACTCTTGAATTTCTACAATGTAGAAATGAGAAATGCCAAATTTGATGGTGA 1620
Db 1561 TATTTACACTCTTGAATTTCTACAATGTAGAAATGAGAAATGCCAAATTTGATGGTGA 1620
QY 1621 TAAAGTCACTGTAAGACAGAGTGAATTTGGTTCATCCAGGCTTTTGTCTTGGTGTTCATG 1680
Db 1621 TAAAGTCACTGTAAGACAGAGTGAATTTGGTTCATCCAGGCTTTTGTCTTGGTGTTCATG 1680
QY 1681 ATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1740
Db 1681 ATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1740
QY 1741 GAAAGTTTCACTGTAAGTGAATTCAGAAATGCTTCAACTGAAAAAACAATATCCAAATA 1800
Db 1741 GAAAGTTTCACTGTAAGTGAATTCAGAAATGCTTCAACTGAAAAAACAATATCCAAATA 1800
QY 1801 ATGAGGAAATGTGTGGCTCACTAGCTAGAGTCCAGAGGAGACAGTCAAGTTTAAAGTTCG 1860
Db 1801 ATGAGGAAATGTGTGGCTCACTAGCTAGAGTCCAGAGGAGACAGTCAAGTTTAAAGTTCG 1860
QY 1861 CTGTATCCAGTAACTCGGGGCTGTTCCTCCCGTGGGCTCTGGGCTGTACAGCTTTCCTTT 1920
Db 1861 CTGTATCCAGTAACTCGGGGCTGTTCCTCCCGTGGGCTCTGGGCTGTACAGCTTTCCTTT 1920
QY 1921 CTCCATGTGTTGATTTCTCTCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACACA 1980
Db 1921 CTCCATGTGTTGATTTCTCTCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACACA 1980
QY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
Db 1981 CAGCAACATCCAGAAATTAAGATCT 2005

RESULT 3
US-10-316-540-11
; Sequence 11, Application US/10316540
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
; FILE REFERENCE: RTS-0471
; CURRENT APPLICATION NUMBER: US/10/316,540
; CURRENT FILING DATE: 2002-12-10.
; NUMBER OF SEQ ID NOS: 156

; SEQ ID NO 11
; LENGTH: 2068
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 143
; OTHER INFORMATION: unknown
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)...(1237)
; us-10-316-540-11

Query Match 97.3%; Score 1950.8; DB 8; Length 2068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1985; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

OY 1 TTGCAGGCTGCTGGGCTAAGGCTGCTCAGTTTCTTCTCAGCGGGGACCTGGGAA 60
Db 24 TTGCAGGCTGCTGGGCTAAGGCTGCTCAGTTTCTTCTCAGCGGGGACCTGGGAA 83
OY 61 GCGCCATGGCACTGAGGCACTCGGCTGTGGAGCTGTCCGGCCCTGGCCCGGCGCT 120
Db 84 GCGCCATGGCACTGAGGCACTCGGCTGTGGAGCTGTCCGGCCCTGGCCCGGCGTN 143
OY 121 TCTGTCTATGCTCTGCTGACTTTCGGGGCGCGTGTGTACGCGTGAGCCGCGCGCT 180
Db 144 TCTGTCTATGCTCTGCTGACTTTCGGGGCGCGTGTGTGTACGCGTGAGCCGCGCGCT 203
OY 181 CCCGCTACGAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 240
Db 204 CCCGCTACGAGCTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 263
OY 241 AGCCGGGGGAGCCCGCTGCTGGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 300
Db 264 AGCCGGGGG - AGCCGGCTGCTGGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 321
OY 301 CCTTCCGGCGGCTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGACGGGAA 360
Db 322 CCTTCCGGCGGCTGTGATGAGAACTCCAGCTGGGCCAGAGATTCTGACGGGAA 381
OY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGT - CAGGAAGCTTTCGCG 418
Db 382 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGT - CAGGAAGCTTTCGCG 441
OY 419 GTTAGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGCCAG 478
Db 442 GTTAGCTGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGCCAG 501
OY 479 AAGTGTGAGATCCGTATGCCCGGCTGATCTCCTGGCTGACTTTGCTGTGTGGCCT 538
Db 502 AAGTGTGAGATCCGTATGCCCGGCTGATCTCCTGGCTGACTTTGCTGTGTGGCCT 561
OY 539 TATGTGTGCACTGGGCAATTAATGGCTTTTGTGACCGCACACGCACTGGGCAAGGTTCA 598
Db 562 TATGTGTGCACTGGGCAATTAATGGCTTTTGTGACCGCACACGCACTGGGCAAGGTTCA 621
OY 599 GGTCAATGATGCAAAATATGTTGGAAGGAACAGACATATTTAAGTCTTTTGTGAAAAAC 658
Db 622 GGTCAATGATGCAAAATATGTTGGAAGGAACAGACATATTTAAGTCTTTTGTGAAAAAC 681
OY 659 TCAGAAATGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGTTGAGCACC 718
Db 682 TCAGAAATGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGTTGAGCACC 741
OY 719 TTTCTATAGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGAGCAATGAACC 778
Db 742 TTTCTATAGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGAGCAATGAACC 801
OY 779 CCAGTTCTAGAGCTGTGATCAAAAGACTGTGACTAAAGTCTGATGAACCTTCCCAATCA 838

Db 802 CCAGTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCA 861
OY 839 GATGAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTGCAGATGTATTTGCCAAGAA 898
Db 862 GATGAGCAGCATGATTTGGCCAGAAATGAAGAGAAGTTTGCAGATGTATTTGCCAAGAA 921
OY 899 GACGAAGGAGAGTGTGTCAAAATCTTTGACGGGCAAGATGCCGTGTGACTCCGGTTCT 958
Db 922 GACGAAGGAGAGTGTGTCAAAATCTTTGACGGGCAAGATGCCGTGTGACTCCGGTTCT 981
OY 959 GACTTTGAGAGGTTGTTCATCATGATCACACAAGAAAGGGGCTCGTTATTCACCAG 1018
Db 982 GACTTTGAGAGGTTGTTCATCATGATCACACAAGAAAGGGGCTCGTTATTCACCAG 1041
OY 1019 TGAGGAGCAGAGCTGAGCCCCCGGCTGCACCTCTGCTTTAAACACCCACCATCCC 1078
Db 1042 TGAGGAGCAGAGCTGAGCCCCCGGCTGCACCTCTGCTTTAAACACCCACCATCCC 1101
OY 1079 TTCTTTCAAAAGGATCCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGG 1138
Db 1102 TTCTTTCAAAAGGATCCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGG 1161
OY 1139 ATTCAAGCCGGAAGAGATTTATCAGCTTAACCTCAGATTAATAATGAAAGTAATAGGT 1198
Db 1162 ATTCAAGCCGGAAGAGATTTATCAGCTTAACCTCAGATTAATAATGAAAGTAATAGGT 1221
OY 1199 AAAAGCTAGTCTTAACCTTCCAGGCCCGGCTCAAGTGAATTGAAATCTGCATTTACA 1258
Db 1222 AAAAGCTAGTCTTAACCTTCCAGGCCCGGCTCAAGTGAATTGAAATCTGCATTTACA 1281
OY 1259 GTGTAGAGTAACACATTAACATTTGATGCATGGAACATGGAAGACAGATTAACAGTGTG 1318
Db 1282 GTGTAGAGTAACACATTAACATTTGATGCATGGAACATGGAAGACAGATTAACAGTGTG 1341
OY 1319 CTACCACTTAATCAAGAAAGATTACAGACTCTGATTTCTACAGTATGATGAATTC 1378
Db 1342 CTACCACTTAATCAAGAAAGATTACAGACTCTGATTTCTACAGTATGATGAATTC 1401
OY 1379 AAAAATGTTATCATTTAGGGCTTTGATTTATAAACTTTGGTACTTATACATAATTAT 1438
Db 1402 AAAAATGTTATCATTTAGGGCTTTGATTTATAAACTTTGGTACTTATACATAATTAT 1461
OY 1439 GGTAGTTATTCGCTTCCAGTTTGCCTGATATATTTGTGATTAAGATPCTTGACTT 1498
Db 1462 GGTAGTTATTCGCTTCCAGTTTGCCTGATATATTTGTGATTAAGATPCTTGACTT 1521
OY 1499 ATATTTGAATGGGTCTAGTGAAGAAAGGAATGATATATCTTGAAGACATCGATATACA 1558
Db 1522 ATATTTGAATGGGTCTAGTGAAGAAAGGAATGATATATCTTGAAGACATCGATATACA 1581
OY 1559 TTTATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAATTTGATGCT 1618
Db 1582 TTTATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAAATGCCACAATTTGATGCT 1641
OY 1619 GATAAAGTCAAGTGAACAGAGATGTTGTTGCCATCCAGGCCCTTTGTGTTGTTCA 1678
Db 1642 GATAAAGTCAAGTGAACAGAGATGTTGTTGCCATCCAGGCCCTTTGTGTTGTTCA 1701
OY 1679 TGATCTCCCTTAAGCACAATCCAAACTTTAGCAACAGTTATCACACTTTGTAATTGGCA 1738
Db 1702 TGATCTCCCTTAAGCACAATCCAAACTTTAGCAACAGTTATCACACTTTGTAATTGGCA 1761
OY 1739 AAGAAAGTTTCAACCTGATTTGAATCAGAATGCCCTTCAACTGAAAAAACATATCCAAA 1798
Db 1762 AAGAAAGTTTCAACCTGATTTGAATCAGAATGCCCTTCAACTGAAAAAACATATCCAAA 1821
OY 1799 TAATGAGGAATGTGTGGCTCACTACGTAGATCCAGAGGACAGTCACTTTTAGGGTT 1858
Db 1822 TAATGAGGAATGTGTGGCTCACTACGTAGATCCAGAGGACAGTCACTTTTAGGGTT 1881
OY 1859 GCCTGTATCCAGTAATCGGGGCTGTTTCCCGTGGGCTCTGTGGGCTGTGACTTTCCT 1918
Db 1882 GCCTGTATCCAGTAATCGGGGCTGTTTCCCGTGGGCTCTGTGGGCTGTGACTTTCCT 1941

[illegible]

```

RESULT 4
US-10-316-540-13
; Sequence 13, Application US/10316540
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
; FILE REFERENCE: RTS-0471
; CURRENT APPLICATION NUMBER: US/10/316,540
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 13
; LENGTH: 2946
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(609)
; US-10-316-540-13

```

Query Match	80.6%;	Score 1616.8;	DB 8;	Length 2946;
Best Local Similarity	91.6%;	Pred. No. 0;		
Matches 1789;	Conservative	0;	Mismatches 2;	Indels 161;
				Gaps 1;
QY 54	CTGGGAAGCGCCATGGACACTGCAGGGCATCTCGTGCCTGGAGCTGTCCGGCCCTGGCCCCG	113		
Db 1	CTGGGAAGCGCCATGGACACTGCAGGGCATCTCGTGCATGGAGCTGTCCGGCCCTGGCCCCG	60		
QY 114	GGCCCGTCTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGGTACGGCGTGACCGG	173		
Db 61	GGCCCGTCTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGGTACGGCGTGACCGG	120		
QY 174	CCCGGCTCCCGTACGAGCTGAGCCGCTTGGCCGGGCAAGCGCTGCTAGTGGCTGGAC	233		
Db 121	CCCGGCTCCCGTACGAGCTGAGCCGCTTGGCCGGGCAAGCGCTGCTAGTGGCTGGAC	180		
QY 234	CTGAAGCAGCCCGCGGGGAGCCGCCCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTG	293		
Db 181	CTGAAGCAGCCCGCGGGGAGCCGCCCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTG	240		
QY 294	CTGAGCCCTTCCGCCCGCGGTGTATCATGGAGAATCTCCAGCTGGGCCAGAGATTCTGAG	353		
Db 241	CTGAGCCCTTCCGCCCGCGGTGTATCATGGAGAATCTCCAGCTGGGCCAGAGATTCTGAG	300		
QY 354	CGGGAATATCCAAAGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTC	413		
Db 301	CGGGAATATCCAAAGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAGCTTTC	360		
QY 414	TGCCGTTAGCTGGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAATTT	473		
Db 361	TGCCGTTAGCTGGCCACGATATCAACTATTGGCTTTGTCA-----	402		
QY 474	GGCAGAAAGTGTGAGAAATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGCTGTGGT	533		
Db 403	-----	402		
QY 534	GGCCTTATGTGTGCACTGGGCATTTAATGCTCTTTTGAACGACACGCACTGGCAAG	593		
Db 403	-----	402		
QY 594	GGTCAGTCATTGATCAAAATATGGTGAAGGAACGACATATTTAAGTTCTTTCTGTGG	653		
Db 403	-----GGTGAAGGAACGACATATTTAAGTTCTTTCTGTGG	439		

OY	654	AAAACTCAGAAATCGAGTCTGTGGGGAAGCACCCTCGAGGACAGAACAATGTTGGATGGTGCA	713
.Db	440	AAAACTCAGAAATGAGTCTGTGGGAAGCACCTTCGAGGACAGAACATGTTGGATGGTGCA	499
OY	714	GCACCTTCTTAATACGACTTACAGAGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATA	773
Db	500	GCACCTTCTTAATACGACTTACAGAGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATA	559
OY	774	GAACCCCAGTCTACGAGCTGCTCATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCC	833
Db	560	GAACCCCGAGTCTACGAGCTGCTCATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCC	619
OY	834	AATCAGATGAGCATGATGATGATTGCCAGAAATGAGAAGAAGTTTGCAGATGATTTGCA	893
Db	620	AATCAGATGAGCATGATGATGATTGCCAGAAATGAGAAGAAGTTTGCAGATGATTTGCA	679
OY	894	AAGAAGACGAAGGCGAGTAGTGCTGTCAAATCTTTGACGGCACAGATGCCGTGTGACTCCG	953
Db	680	AAGAAGACGAAGGCGAGTAGTGCTGTCAAATCTTTGACGGCACAGATGCCGTGTGACTCCG	739
OY	954	GTTCTGACTTTTGAAGGAGGTTGTTTCATCATGATCACAACAAGAAACGGGGCTCGTTATC	1013
Db	740	GTTCTGACTTTTGAAGGAGGTTGTTTCATCATGATCACAACAAGAAACGGGGCTCGTTATC	799
OY	1014	ACCAATGAGAGAGACGAGCTGAGCCCCCGCCCTGCACCTCTGTGTTAAACACCCACGCC	1073
Db	800	ACCAATGAGAGAGACGAGCTGAGCCCCCGCCCTGCACCTCTGTGTTAAACACCCACGCC	859
OY	1074	ATCCCTTCTTCAAAAAGGAGTCTTTCATAGAGAAACACACTGAGGAGATACTTGAAGAA	1133
Db	860	ATCCCTTCTTCAAAAAGGAGTCTTTCATAGAGAAACACACTGAGGAGATACTTGAAGAA	919
OY	1134	TTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACTCAGATPAAATCATTTGAAAAGTAT	1193
Db	920	TTTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACTCAGATPAAATCATTTGAAAAGTAT	979
OY	1194	AAGGTAAAGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAACTACTGCAT	1253
Db	980	AAGGTAAAGCTAGTCTCTAATCTCCAGGCCACAGGCTCAAGTGAATTTGAACTACTGCAT	1039
OY	1254	TTACAGTGTAGAGTAACTACATACTGTATGCATGGAAACATGGAGAACACTATTACA	1313
Db	1040	TTACAGTGTAGAGTAACTACATACTGTATGCATGGAAACATGGAGAACACTATTACA	1099
OY	1314	GTTGCTTACCACTCTAATCAAGAAAGAATTTACAGACTCTGATCTACAGTSGATGATTGA	1373
Db	1100	GTTGCTTACCACTCTAATCAAGAAAGAATTTACAGACTCTGATCTACAGTSGATGATTGA	1159
OY	1374	ATTCTAAAAATGTTATCATTTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAA	1433
Db	1160	ATTCTAAAAATGTTATCATTTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAA	1219
OY	1434	ATTATGAGTAGTATTCTGCGCTTCCAGTTTGCTTGATATATTGTTGATATTAGATTCTT	1493
Db	1220	ATTATGAGTAGTATTCTGCGCTTCCAGTTTGCTTGATATATTGTTGATATTAGATTCTT	1279
OY	1494	GACTTATATTTTGAATGGGTTCTAGTGAAAAAAGAAATGATATATCTTGAAGACATCGAT	1553
Db	1280	GACTTATATTTTGAATGGGTTCTAGTGAAAAAAGAAATGATATATCTTGAAGACATCGAT	1339
OY	1554	ATACATTTATTTTACACTCTTGATTTCTACAAATGTAGAAAAATGAGGAAATGCCACAATTTGT	1613
Db	1340	ATACATTTATTTTACACTCTTGATTTCTACAAATGTAGAAAAATGAGGAAATGCCACAATTTGT	1399
OY	1614	ATGGTGATATAAAGTCACGTCGAACACAGAGTATGGTTGCATCCAGGCCCTTTGTCTTGGT	1673
Db	1400	ATGGTGATATAAAGTCACGTCGAACACAGAGTATGGTTGCATCCAGGCCCTTTGTCTTGGT	1459
OY	1674	GTTCATGATCTCCCTTAAGCACAATTTCCAACCTTTAGCAACAGTTATCACACTTTGTAAT	1733
Db	1460	GTTCATGATCTCCCTTAAGCACAATTTCCAACCTTTAGCAACAGTTATCACACTTTGTAAT	1519

QY 1734 TTGCAAGAAAGTTTCACTGTATGTGATCAGAAATGCGCTTCACTGAAAAACATATC 1793
|||||
Db 1520 TTGCAAGAAAGTTTCACTGTATGTGATCAGAAATGCGCTTCACTGAAAAACATATC 1579
QY 1794 CAAAATATAGGAATGTGTGGCTCAGTACGTAGAGTCCAGAGGAGCAGTCACTTTTA 1853
|||||
Db 1580 CAAAATATAGGAATGTGTGGCTCAGTACGTAGAGTCCAGAGGAGCAGTCACTTTTA 1639
QY 1854 GGGTGGCTGTATCCAGTAACTCGGGGCGCTTTCCCGTGCGTCTGTGGGCTGTACGCT 1913
|||||
Db 1640 GGGTGGCTGTATCCAGTAACTCGGGGCGCTTTCCCGTGCGTCTGTGGGCTGTACGCT 1699
QY 1914 TTCCTTCTCCATGTGTGTGATTTCTCCTCAGGCTGTAGCAAGTTCTGTGATCTTATACC 1973
|||||
Db 1700 TTCCTTCTCCATGTGTGTGATTTCTCCTCAGGCTGTAGCAAGTTCTGTGATCTTATACC 1759
QY 1974 CAACACACAGCAACATCCAGAATAAGTCT 2005
|||||
Db 1760 CAACACACAGCAACATCCAGAATAAGATCT 1791

RESULT 5

US-09-593-793A-107
; Sequence 107, Application US/09593793A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Helper, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42715C15
; CURRENT APPLICATION NUMBER: US/09/593,793A
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-593-793A-107

Query Match 78.5%; Score 1574.2; DB 6; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGGTGAGAGCTGTCCGGCTGGCCCGGGCGCTT 121
|||||
Db 1 CGCCATGGCACTGCAGGGCATCTCGGTGAGAGCTGTCCGGCTGGCCCGGGCGCTT 60
QY 122 CTGTGCTATGCTCTGCTGACTTCCGGGCGGTGTGACGCGTGACCGCGCGGCTC 181
|||||
Db 61 CTGTGCTATGCTCTGCTGACTTCCGGGCGGTGTGACGCGTGACCGCGGCTC 120
QY 182 CCGCTAGCAGCTGAGCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA 241
|||||
Db 121 CCGCTAGCAGCTGAGCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGAGCTGAAGCA 180
QY 242 GCCGGGGGAGCCCGCTGCTGCGGCGTGTGTGCAAGCGGTGGATGTGCTGTGAGACC 301
|||||

Db 181 GCCCGGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGTGAGCC 240
QY 302 CTTCCGGCGGGGTGTCAATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAA 361
|||||
Db 241 CTTCCGGCGGGGTGTCAATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAA 300
QY 362 TCCAAGGCTTATTATGCGAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCGGTT 421
|||||
Db 301 TCCAAGGCTTATTATGCGAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCGGTT 360
QY 422 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGTGTCTCTCAAAAAATTGCGAAG 481
|||||
Db 361 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGTGTCTCTCAAAAAATTGCGAAG 420
QY 482 TGGTGAAGATCCGTATGCCCCGCTGAATCTCGTGGCTGACTTTGCTGTGGTGGCTTAT 541
|||||
Db 421 TGGTGAAGATCCGTATGCCCCGCTGAATCTCGTGGCTGACTTTGCTGTGGTGGCTTAT 480
QY 542 GTGTGCACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGT 601
|||||
Db 481 GTGTGCACTGGGCATTATTAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGT 540
QY 602 CATGTATGCAATATGTGTGAAGGAACAGCATATTAAGTCTTTTCTGTGAAAACTCA 661
|||||
Db 541 CATGTATGCAATATGTGTGAAGGAACAGCATATTAAGTCTTTTCTGTGAAAACTCA 600
QY 662 GAAATCGAGTCTGTGGAGCACTCGAGGACAGACATGTGTGATGTGTGAGCACTTT 721
|||||
Db 601 GAAATCGAGTCTGTGGAGCACTCGAGGACAGACATGTGTGATGTGTGAGCACTTT 660
QY 722 CTATACGACTTACAGAGCAGCAGATGGGAATTTCAGCTGTGGCAATAGAACCCCA 781
|||||
Db 661 CTATACGACTTACAGAGCAGCAGATGGGAATTTCAGCTGTGGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 841
|||||
Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTGCAGATGTATTGCAAGAAGAC 901
|||||
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTGCAGATGTATTGCAAGAAGAC 840
QY 902 GAAGGCAAGTGTGTCAAACTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGAC 961
|||||
Db 841 GAAGGCAAGTGTGTCAAACTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGAC 900
QY 962 TTTTGGAGAGTGTGTTCATCATGATCACAACAAGAACGGGCTCGTTTATCACAGTGA 1021
|||||
Db 901 TTTTGGAGAGTGTGTTCATCATGATCACAACAAGAACGGGCTCGTTTATCACAGTGA 960
QY 1022 GGAGCAGAGCGTAGCCCCCGCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTC 1081
|||||
Db 961 GGAGCAGAGCGTAGCCCCCGCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCCTTTCATAGGAGAACACACACTGAGAGATACTTGAAGAAATTGGATT 1141
|||||
Db 1021 TTTCAAAAGGATCCTTTCATAGGAGAACACACACTGAGAGATACTTGAAGAAATTGGATT 1080
QY 1142 CAGCCCGGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGTTAA 1201
|||||
Db 1081 CAGCCCGGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGTTAA 1140
QY 1202 AGCTAGTCTTAATTCAGGCCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1261
|||||
Db 1141 AGCTAGTCTTAATTCAGGCCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1200
QY 1262 TAGAGTAACACATTAATTTATGATGGAACATGAGGAACAGATATACAGTGTCTTA 1321
|||||
Db 1201 TAGAGTAACACATTAATTTATGATGGAACATGAGGAACAGATATACAGTGTCTTA 1260
QY 1322 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGATGATTAATTTCTAAA 1381
|||||
Db 1261 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGATGATTAATTTCTAAA 1320

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OY 1382 AAGGTTATCATATGAGGCTTTTGATTTTATAAAACCTTTGGGTACTATATCTAAATATGCT 1441
      |||||||
Db 1321 AATGCTTATCATATGAGGCTTTTGATTTTATAAAACCTTTGGGTACTATATCTAAATATGCT 1380
      |||||||
OY 1442 AGTATTTCTGCGCTTCCAGTTTGCTTGATATATTTGTTGATATATAGATTCTTGACTTATA 1501
      |||||||
Db 1381 AGTATTTCTGCGCTTCCAGTTTGCTTGATATATTTGTTGATATATAGATTCTTGACTTATA 1440
      |||||||
OY 1502 TTTTGATGCGGTTCTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1561
      |||||||
Db 1441 TTTTGATGCGGTTCTAGTGAAGAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 1500
      |||||||
OY 1562 ATTACACTCTTGATTTCTACAAATGTAAGAAATGAGGAATGCCACAATTTGATGCTGAT 1621
      |||||||
Db 1501 ATTACACTCTTGATTTCTACAAATGTAAGAAATGAGGAATGCCACAATTTGATGCTGAT 1560
      |||||||
OY 1622 AAAAGTCACGTGAACAGA 1640
      |||||||
Db 1561 AAAAGTCACGTGAACAGAA 1579
      |||||||

RESULT 6
US-10-294-025-107
; Sequence 107, Application US/10294025
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294, 025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-107

```

Query Match	78.5%;	Score 1574.2;	DB 8;	Length 1621;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1576;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;
QY	62	CGCCATGGCACTGCAGGGGCATCTGCGTCTGGAGCTGTCCGGCTGGCCCCGGGCCGTT	121	
Db	1	CGCATGGCACTGCAGGGGCATCTGCGTCTGGAGCTGTCCGGCTGGCCCCGGGCCGTT	60	
QY	122	CTGTGCTATGGTCTGCTGGCTGACTTCGGGGCGCGTGTGTACGCGCTGGACCCGGCCCGCTC	181	
Db	61	CTGTGCTATGGTCTGCTGGCTGACTTCGGGGCGCGTGTGTGTACGCGCTGGACCCGGCCCGCTC	120	
QY	182	CCGCTACGACGTGAGCCCGCTTGGGCCGGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA	241	
Db	121	CCGCTACGACGTGAGCCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCA	180	
QY	242	GCCGCGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGAATGTGCTGTGAGGCC	301	
Db	181	GCCGCGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGAATGTGCTGTGAGGCC	240	
QY	302	CTTCCGCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCAGAGATTTCTGCAGCGGAAAA	361	
Db	241	CTTCCGCGCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCAGAGATTTCTGCAGCGGAAAA	300	
QY	362	TCCAAGGCTTATTTATGCGCAGGCTGAGTGGATTGGCCAGTCAAGAAAGCTTCTGCCGGTT	421	
Db	301	TCCAAGGCTTATTTATGCGCAGGCTGAGTGGATTGGCCAGTCAAGAAAGCTTCTGCCGGTT	360	
QY	422	AGCTGGCCACGATATCAACTAATTTGGCTTTGTCAAGGTGTTCTCTCAAAAAATTGGCAGAAG	481	
Db	361	AGCTGGCCACGATATCAACTAATTTGGCTTTGTCAAGGTGTTCTCTCAAAAAATTGGCAGAAG	420	

QY	482	TGGTGAGAAATCCCGTATATGCCCCCGCTGAATCTCTCGGCTGACTTTGCTGTGGTGGCCCTTAT	541
Db	421	TGGTGAGAAATCCCGTATATGCCCCCGCTGAATCTCTCGGCTGACTTTGCTGTGGTGGCCCTTAT	480
QY	542	GTGTGCACTGGGCATTTATATAGCGCTTTTGTGACCCGCACACGCACACTGGCAAGGGTCAGGT	601
Db	481	GTGTGCACTGGGCATTTATATATAGCGCTTTTGTGACCCGCACACGCACACTGGCAAGGGTCAGGT	540
QY	602	CATTGATGCAAAATATGGTGGAAAGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA	661
Db	541	CATTGATGCAAAATATGGTGGAAAGAAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA	600
QY	662	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT	721
Db	601	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT	660
QY	722	CTATACGACTTACAGAGACAGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	781
Db	661	CTATACGACTTACAGAGAGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCA	720
QY	782	GTTTCTACGAGCTGCTGATCAAAAGCACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT	841
Db	721	GTTTCTACGAGCTGCTGATCAAAAGCACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT	780
QY	842	GAGCATGGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAGAAGAGAC	901
Db	781	GAGCATGGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAGAAGAGAC	840
QY	902	GAAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTCTGAC	961
Db	841	GAAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTCTGAC	900
QY	962	TTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGTGGTTATGACCAGTGA	1021
Db	901	TTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGTGGTTATGACCAGTGA	960
QY	1022	GGAGCAGAGCGTGAGCCCCCGCCCTGCACCTGTGCTGTTAAACACCCCAAGCCATCCCTTC	1081
Db	961	GGAGCAGAGCGTGAGCCCCCGCCCTGCACCTGTGCTGTTAAACACCCCAAGCCATCCCTTC	1020
QY	1082	TTTTCAAAAGGAGTCCCTTTCATAGAGAGAACACACTGAGAGATCTTGAAGAAATTTGGATT	1141
Db	1021	TTTTCAAAAGGAGTCCCTTTCATAGAGAGAACACACTGAGAGATCTTGAAGAAATTTGGATT	1080
QY	1142	CAGCCGCGAAGAGATTTTATCAGCTTTAACTCAGATAAATCATTTGAAGTAATTAAGTAAA	1201
Db	1081	CAGCCGCGAAGAGATTTTATCAGCTTTAACTCAGATAAATCATTTGAAGTAATTAAGTAAA	1140
QY	1202	AGCTAGTCTCTAACTTCCAGGCCCCAGGCTCAAGTGAATTTGAATACTGCATTTTACAGTG	1261
Db	1141	AGCTAGTCTCTAACTTCCAGGCCCCAGGCTCAAGTGAATTTGAATACTGCATTTTACAGTG	1200
QY	1262	TAGAGTAACACATTAACATTTGTATGCATGGAACATGGAGAACAGTATTACAGTGTCTTA	1321
Db	1201	TAGAGTAACACATTAACATTTGTATGCATGGAACATGGAGAACAGTATTACAGTGTCTTA	1260
QY	1322	CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA	1381
Db	1261	CCACTCTAATCAAGAAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAAA	1320
QY	1382	AATGCTTATCATTAAGGGCTTTTGAATTTTATAAAACTTTGGGTACTTATACTAAATTAATGTGT	1441
Db	1321	AATGCTTATCATTAAGGGCTTTTGAATTTTATAAAACTTTGGGTACTTATACTAAATTAATGTGT	1380
QY	1442	AGTATATTTCTGCCTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATA	1501
Db	1381	AGTATATTTCTGCCTCCAGTTTGGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTATA	1440
QY	1502	TTTTGAATGGGTTCTAGTGA AAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT	1561
Db	1441	TTTTGAATGGGTTCTAGTGA AAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT	1500

DB	1501	ATTACACCTCTGATTCTACATGTAGAAATGAGAAATGCCCAATTTGATGGTGAT	1560
QY	1622	AAAAGTCACGTGAACAGA	1640
DB	1561	AAAAGTCACGTGAACAAA	1579

RESULT 8

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US-10-316-540-4
: Sequence 4, Application US/10316540
: GENERAL INFORMATION:
: APPLICANT: Kenneth W. Doble
: APPLICANT: Ravi Jain
: TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
: FILE REFERENCE: RTS-0471
: CURRENT APPLICATION NUMBER: US/10/316,540
: CURRENT FILING DATE: 2002-12-10
: NUMBER OF SEQ ID NOS: 156
: SEQ ID NO 4
: LENGTH: 21814
: TYPE: DNA
: ORGANISM: H. sapiens
: FEATURE:
US-10-316-540-4

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Query Match	59.9%;	Score 1201.4;	DB 8;	Length 21814;
Best Local Similarity	99.9%;	Pred. No. 5e-287;		
Matches 1202; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0

QY	803	AGGACTTGGACTAAAGTCTGATGAACTCCCAATCAGATGAGCATGATGATTTGGCCAGA	862
Db	19084	AGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGATGATTTGGCCAGA	19143
QY	863	AATCAGAAGAAGTTTGCAGATGTATTTGCCAAAAGAAGACGAAGGCAGAGTGTGTCAAAAT	922
Db	19144	AATCAGAAGAAGATTTCAGATGTATTTGCCAAAAGAAGACGAAGGCAGAGTGTGTCAAAAT	19203
QY	923	CTTTGACGGCACAGATGCGCTGTGTGACTCCGGTCTGTGACTTTTGAGGAGTGTGTTATCA	982
Db	19204	CTTTGACGGCACAGATGCGCTGTGTGACTCCGGTCTGTGACTTTTGAGGAGTGTGTTATCA	19263
QY	983	TGATCACAACAAGAACGGGGGCTCGTTTATCACCAGTAGAGAGCAGAGCCTGAGCCCCCG	1042
Db	19264	TGATCACAACAAGAACGGGGGCTCGTTTATCACCAGTAGAGAGCAGAGCCTGAGCCCCCG	19323
QY	1043	CCCTGCACCTCTGCTGTTAACACACCCACGCCATCCCTCTTTCAAAAGGATCCTTCAT	1102
Db	19324	CCCTGCACCTCTGCTGTTAACACACCCACGCCATCCCTCTTTCAAAAGGATCCTTCAT	19383
QY	1103	AGGAGAACACACACTGAGGAGATACTTGAAGAATTTGGATTCAAGCCGGAAGAGATTATCA	1162
Db	19384	AGGAGAACACACACTGAGGAGATACTTGAAGAATTTGGATTCAAGCCGGAAGAGATTATCA	19443
QY	1163	GCCTTAACCTCAGATAAAAATCATTGAAAGTAATTAAGGTAAAAAGCTAGTCTCTAACTTCCAGG	1222
Db	19444	GCCTTAACCTCAGATAAAAATCATTGAAAGTAATTAAGGTAAAAAGCTAGTCTCTAACTTCCAGG	19503
QY	1223	CCACAGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACACATAACATTGT	1282
Db	19504	CCACAGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACACATAACATTGT	19563
QY	1283	ATGCATGGAACATGAGAGGAACAAGTATTACAGTGTCTAACCACTCTAATCAGAAAAAGAA	1342
Db	19564	ATGCATGGAACATGAGAGGAACAAGTATTACAGTGTCTAACCACTCTAATCAGAAAAAGAA	19623
QY	1343	TTACAGACTCTGATTCCTACAGTGAATTTGAATTTCTAAAAATGTTATTATCAATTAGGGCTTT	1402
Db	19624	TTACAGACTCTGATTCCTACAGTGAATTTGAATTTCTAAAAATGTTATTATCAATTAGGGCTTT	19683
QY	1403	TGATTTATTAACCTTTGGGTACTTATACTAAATTAATGAGTATATTCGTGCCCTTCCAGTTT	1462
Db	19684	TGATTTATTAACCTTTGGGTACTTATACTAAATTAATGAGTATATTCGTGCCCTTCCAGTTT	19743

QY	1463	GCCTGATATATTTGTTGCATATTAAGATCTTGACTTATATTTTGAATGGGTCTAGTAA	1522
Db	19744	CGTCGATATATTTTGTTCGATATTAAGATCTTGACTTATATTTTGAATGGGTCTAGTAA	19803
QY	1523	AAAGCAATGATATATCTTGAAGACATCGATATACATTTATTTACACTCTTGATTCTACA	1582
Db	19804	AAAGCAATGATATATTTCTTGAAGACATCGATATACATTTATTTACACTCTTGATTCTACA	19863
QY	1583	ATGTAGAAAATGAGAAATGCCACAATTTGTATGTTAAAGTCACGTGAAACAGAGT	1642
Db	19864	ATGTAGAAAATGAGAAATGCCACAATTTGTATGTTAAAGTCACGTGAAACAGAGT	19923
QY	1643	GATTGGTTGCATCCAGGCCCTTTTGTCTGGGTGTTCAATGATCTCCCTCTAAGCACATTCCA	1702
Db	19924	GATTGGTTGCATCCAGGCCCTTTTGTCTGGGTGTTCAATGATCTCCCTCTAAGCACATTCCA	19983
QY	1703	AACCTTACGACACAGTTATCCACACTTTGTATTTTGCAAAAGAAAAGTTTCACCTGTATTGAA	1762
Db	19984	AACCTTACGACACAGTTATCCACACTTTGTATTTTGCAAAAGAAAAGTTTCACCTGTATTGAA	20043
QY	1763	TCAGATGCGCTTCAACTGAAAAAAACATATCCAAAAATTAATGAGGAAATGTGTGGCTCAC	1822
Db	20044	TCAGATGCGCTTCAACTGAAAAAAACATATCCAAAAATTAATGAGGAAATGTGTGGCTCAC	20103
QY	1823	TACGTAGAGTCCAGAGGACAGTCAGTTTAAAGGTGCGCTGATCCAGTAACCTCGGGGCC	1882
Db	20104	TACGTAGAGTCCAGAGGACAGTCAGTTTAAAGGTGCGCTGATCCAGTAACCTCGGGGCC	20163
QY	1883	TGTTTCCCGGTGGGTCTCTGGGCTGTACAGCTTTCCTTCTCCATGTGTGATTCTCCCT	1942
Db	20164	TGTTTCCCGGTGGGTCTCTGGGCTGTACAGCTTTCCTTCTCCATGTGTGATTCTCCCT	20223
QY	1943	CAGGCTGGTAGCAAGTCTCGATCTTATATCCCAACACACAGCAACATCCAGAAATAAGT	2002
Db	20224	CAGGCTGGTAGCAAGTCTCGATCTTATATCCCAACACACAGCAACATCCAGAAATAAGT	20283
QY	2003	TCT 2005	
Db	20284	TCT 20286	

RESULT 9

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: Sequence 3147, Application PC/TUS0303482
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Higgs, Brandon
: APPLICANT: Castle, Arthur
: APPLICANT: Orr, Michael
: APPLICANT: Elashoff, Michael
: TITLE OF INVENTION: Primary Rat Hepatocyte Toxicity Modeling
: FILE REFERENCE: 44921-5113-WO
: CURRENT APPLICATION NUMBER: PCT/US03/03482
: CURRENT FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 60/353,171
: PRIOR FILING DATE: 2002-02-04
: PRIOR APPLICATION NUMBER: 60/363,534
: PRIOR FILING DATE: 2002-03-15
: PRIOR APPLICATION NUMBER: 60/371,135
: PRIOR FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: 60/371,134
: PRIOR FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: 60/370,248
: PRIOR FILING DATE: 2002-04-08
: PRIOR APPLICATION NUMBER: 60/371,150
: PRIOR FILING DATE: 2002-04-10
: PRIOR APPLICATION NUMBER: 60/371,413
: PRIOR FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/373,601
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: 60/374,139

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; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/394,253
; PRIOR FILING DATE: 2002-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4486
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3147
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
PCT-US03-03482-3147

Query Match          41.4%; Score 830; DB 1; Length 1504;
Best Local Similarity 76.3%; Pred. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

QY 72 CTGCAGGCGATCTGGTCTGTGAGCTGTCCGGCTGGCCCCGGCCGCTTCGTCTATG 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 CTGCGTGGCGTCAAGGTTCTGAGCTGGCAGGCCCTGGCCCCAGGGCGTTCGGGGATG 61

QY 132 GTCTGGCTGACTTCGGGGCGCGGTGTGTAGCGCTGGACCGCGCCGCTCCCGCTACGAC 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 ATCCTGGCGACTTCGGCGCCGCGAGGTGTGTCTCTGTGACAGACTGGGCTCCGTGAACAC 121

QY 192 GTGAGCCGCTTGGGGCGGGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCAGCGCGGGGA 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 CCCAGTCACTGGCCCGAGGCAAGCGCTCGCTGGCGCTGGACCTGAAGCGGTCTCCGGGA 181

QY 252 GCCGCCGTGTGGCGGCTGTGTCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GCCGCGGTGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241

QY 312 GGTGTATGAGAACTCCAGCTGGGCCAGAGATCTGCAGCGGAAATCCAAAGCTT 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 GGTGTATGAGAACTCCAGCTGGGCCAGAGATCTGCAGCGGAAATCCAAAGCTT 301

QY 372 ATTTATGCCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 ATCTATGCCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 361

QY 432 GATATCACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAT 491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GACATCACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAGTGTGAGAT 421

QY 492 CCGTATGCCCGCTGATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 CCATACCTCCCTGAACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481

QY 552 GGCATTATATGCTCTTTTGTACCCGACACGCACTGGCAAGGTCAGGTCAATTGATGA 611
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 GGCATTATATGCTCTTTTGTACCCGACACGCACTGGCAAGGTCAGGTCAATTGATGA 541

QY 612 AATATGTTGAAGGACAGCATATTTAAGTTCTTTCTGTGAAAACCTCAGAAATCGAGT 671
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 AACATGTTGAAGGACAGCATATTTAAGTTCTTTCTGTGAAAACCTCAGGCAATGGGT 601

QY 672 CTGTGGAAGCACTCGAGGACAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 731
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 CTGTGGAAGCACTCGAGGACAGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 661

QY 732 TACAGGACAGCATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCAGTTCTACGAG 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 662 TACAGGACAGCATGGGGAATTCATGGCTGTGTGAGCAATAGAACCCAGTTCTACACA 721

QY 792 CTGCTGATCAAGGACTTGACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGAT 851
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 722 CTGCTGATCAAGGACTTGACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATAGAA 781

QY 852 GATTGGCCAGAAATGAGAAGAGTTTGCAGATGTATTGCAAGAAGAGAGAGAGAGAG 911
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 782 GATTGGCCAGAAATGAGAAGAGTTTGCAGATGTATTGCAAGAAGAGAGAGAGAGAG 841

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QY 912 TGGTCAATCTTTGACGGCACAGATGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 842 TGGTCCAGATCTTTGACGGGACAGATGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901

QY 972 GTTGTTCATCATGATCAACAAGAGAACGGGGCTGTATTATCACCAGTGAAGAGCAGGAC 1031
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 902 GCCCTCCACCACAGACACAGAGAACGGGGCTGTATTATCACCAGTGAAGAGCAGCAT 961

QY 1032 GTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCAAGCCATCCCTTCTTCAAAAG 1091
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 962 GCATGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCAAGCCATCCCTTCTTCAAAAG 1021

QY 1092 GATCCTTTCATAGAGACACACACTGAGAGATCTTGAAGATTTGGATTTCAGCCCGGAA 1151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1022 GACCTTCTGTGGAGAGACACACTGTAGAGGTGCTTAAAGACTATGATTTCAGTCAAGAA 1081

QY 1152 GAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAAAGTAAAGCTAGTCTC 1211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1082 GAGATTCATCAGCTTGACTCGGATAGATCATTTGAAGTAAAGTAAAGCTAAAGCCAACTC 1141

QY 1212 TAACCTCCAGGCCCGCTCAAGTGAATTTGAATTAAGTATTAAGTGTAGAGTAACA 1271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1142 TGAAT - CAGGTTACAGCTCAAGTGAATTTGAAGTGTAGTGTAGTGTAGAGATG 1199

QY 1272 CATAACATTTGATGATGAACATGAGAGAACATTAAGTGTCTTACAGTCTTAAT 1331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1200 CCCACCACTGTCCGTTGAAGTGAATGTAATGAAGTAAATCCAAATATTCCAA 1259

QY 1332 CAAGAAAGATTTACAGACTGTGATTTCTACAGTGTATGATTTCTAAATAGTTATC 1391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1260 TCAAGACACACGAAGA - CTGATTACAGAGAAATGACTGTGTCTACACCTCATC 1317

QY 1392 ---ATTAGGCTTTGATTTATAAACTTTGGGTACTTACTAAATTTAGTATTTAT 1448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1318 CGAGCCTCTGATTGAGAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376

QY 1449 CTGCTTCAGTTTGTGTATATT 1474
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1377 CTGCTTTCAGCTTACTTGTGTAAGT 1402

RESULT 10
PCT-US03-03194-3149
; Sequence 3149, Application PC/TUS0303194
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-01-WO
; CURRENT APPLICATION NUMBER: PCT/US03/03194
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459

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; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; PRIOR FILING DATE: 2001-11-13
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4295
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3149
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
PCT-US03-03194-3149

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Query Match      41.4%; Score 830; DB 1; Length 1504;
Best Local Similarity 76.3%; Pred. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

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QY 72 CTGACGGGACATCTCGGTCTGTGAGCTGTCCGGCCTGGCCCCCGGGCCGCTCTGTGCTATG 131
Db 2 CTGCGTGGCGTCAAGGCTTCTGTGAGCTGTGAGCGCTGGCCCCAGGAGGCGCTTCTGCGGGATG 61
QY 132 GTCTGTGCTGACTTTCGGGGCGCGCTGTGTGACGCTGTGAGCCGCGCGCTCCGCTACGAC 191
Db 62 ATCTGTGGCGGACTTTCGGCGCGCGAGGCTGTGTGTGTGACAGACTGGGCTCCGTGAACCAAC 121
QY 192 GTGAGCCGCTTGGGCGCGCGAGCCGCTCGCTACTGCTGTGAGCTGTGAGCAGCCGCGGGA 251
Db 122 CCAAGTCACTGCGCGCGAGGAGGAGCGCTCGCTGCGCGCTGTGAGCTGTGAGCGGCTCCGGA 181
QY 252 GCCGCGCTGTGCTGCGCGCTGTGTGCAAGCGGTGATGTGTGTGTGAGCGCTTCCGCGC 311
Db 182 GCGCGGCTGTGTGCGCGCATGTGTGCGCAGCGCGCGAGCGTGTGTGTGAGCGCTTCCGTTGC 241
QY 312 GGTGTGATGAGAACTCCAGCTGGGCGCGCAGAGATTCTGTGAGCGGGAATCCAGGCTT 371
Db 242 GGTGTGATGAGAACTCCAGCTTGGGCGCAGAGACTCTACGGCAGGACAATCCAAAGCTC 301
QY 372 ATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAAGCAAGCTTCCCGGTTAGCTGGCCAC 431
Db 302 ATCTATGCCAGGCTGAGTGTGATTTGGCCAGTCAAGCAAGCTTCCAAAGTAGCTGGCCAT 361
QY 432 GATATCACTATTGGCTTGTGTGAGGTGTCTCTCAAAAATTTGCGAGAGAGTGTGAGAA 491
Db 362 GACATCACTATGTGGCTTGTGTGAGGTGTCTCTCAAAAGATTGCGAGAGCGGTGAGAAC 421
QY 492 CCGTATGCCCGCTGATCTCCGTGGCTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
Db 422 CCATACCCCTCCCTGAACCTCGTGGCGGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481
QY 552 GGCATTTATATGCTCTTTTGTGACCGCACAGCAGCTGTGCAAGGCTCAGTCAATGTATGCA 611
Db 482 GGCATTTTGTGCTCTCTTGTGACCGCACAGCAGCGGTGTGCGCTAGGCGAGTCAATGTATGCG 541
QY 612 AATATGTTGGAAGAGACAGCATATTTAAGTCTTTTCTGTGTGAAACTCAGAAATCGAGT 671
Db 542 AACATGTTGGAAGAGACAGCATATTTAAGTCTTTTCTGTGTGAAACTCAGAGGCGATGGGT 601
QY 672 CTGTGGGAAGACACTCGAGAGACAGACATGTGTGATGTGTGAGACACTTCTATACGACT 731
Db 602 CTGTGGGACACAGCCTCGAGGCAAACTGTATGATGGCGGCGACCTTCTACACAACC 661
QY 732 TACAGGACAGCAGATGGGAATTCAGTGTGTGTGAGCAATAGAACCCAGTTCATACGAG 791
Db 662 TACAAGACCGCAGATGGGAGTTCATGTGTGTGATGTGCAATAGAACCCAGTTCATACACA 721
QY 792 CTGCTGATCAAGAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGATGAT 851
Db 722 CTGCTGCTTAAAGAGACTTGGACTTGAAGTCTGAGGAACTCCCGCAGCAGATGAGCATAGAA 781
QY 852 GATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGAGAGAGAGAGAGAG 911
Db 782 GATTGGCCAGAAATGAAGAAGTTTGCAGATGTGTGTGCAAGAAGAGAGACTAAGCAGAGAG 841

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QY 912 TGGTCAAACTTTGACGGCACAGATGCGCTGTGTGACTCCGGTCTGTGACTTTTGAGAG 971
Db 842 TGGTCCAGACTCTTTGACGGGACAGATGATGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAG 901
QY 972 GTTGTTCATCATGATCACAACAAGAACGGGCTGTTTATCACCAGTGTGAGGAGAGAGAC 1031
Db 902 GCGCTTCACACACAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 961
QY 1032 GTGAGCCCCCGCCCTGACCTCTGCTGTTAACACACCCACCATCCCTCTTTCAAAAGG 1091
Db 962 GCATGCCCCCGCTCTGACCCCAAGCTTTCAGAGAACCCCTGCTGTCTCTTCCCAAAAGG 1021
QY 1092 GATCCTTTTATAGAGAACACACTGAGAGATACTTGAAGAATTTGATTCAGCCGCGAA 1151
Db 1022 GACCCCTTCTGTGGAGAGACACTGTAGAGGTGCTTAAAGACTATGATTCAGTCAAGGAA 1081
QY 1152 GAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAAATGAGTAAAGCTAGTCTC 1211
Db 1082 GAGATTCATCAGCTGTGACACTCGGATAGAAATCATTTGAAAGTAAATGAGTAAAGCCAACTTC 1141
QY 1212 TAACCTCCAGGCCCGCTCAAGTGAATTTGAATACATGATTTACAGTGTAGAGTAA 1271
Db 1142 TGACT--CAGGTTACACAGCTCAAGTGAATGTGAAGGCTGTATCTGTACTGTGAGAGATG 1199
QY 1272 CATAACATGTATGATGAGAAACATGAGAGACAGTATTAACAGTGTCTTACCACCTTAAT 1331
Db 1200 CCGCACCCTGTCCGATGAGAAATGTGAATGAACAGTAAATGAAGTAAATCAATATTCCAA 1259
QY 1332 CAAGAAAGAAATTACAGACTGTATCTACAGTGTATGATGATGATGATGATGATGATGATG 1391
Db 1260 TCAAGACACACGAAGA--CTGATTACAGAGAAATGACTGTGCTCTCACACTGCTCATC 1317
QY 1392 ---ATTAGGCTTTGATTATTAACCTTTGGGTACTTATTAATAATTATGTTAGTTAT 1448
Db 1318 CGAGCCTCTGATTTGAGAGATATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376
QY 1449 CTGCTTCCAGTTTGTGTGATATTT 1474
Db 1377 CTGCTTTCAGCTTACTTGTGTAAGT 1402

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RESULT 11
US-10-152-319A-1546
: Sequence 1546, Application US/10152319A
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Higgs, Brandon
: APPLICANT: Castle, Arthur
: APPLICANT: Elashoff, Michael
: TITLE OF INVENTION: Molecular Toxicology Modeling
: FILE REFERENCE: 44921-5089-US
: CURRENT APPLICATION NUMBER: US/10/152,319A
: PRIOR FILING DATE: 2002-05-22
: PRIOR APPLICATION NUMBER: US 60/292,335
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/297,523
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,925
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,810
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/303,807
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/303,808
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/315,047
: PRIOR FILING DATE: 2001-08-28
: PRIOR APPLICATION NUMBER: US 60/324,928
: PRIOR FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: US 60/330,867

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; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1546
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-152-319A-1546

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Query Match	41.48;	Score 830;	DB 8;	Length 1504;
Best Local Similarity	76.38;	Pred. No. 2e-195;		
Matches 1073; Conservative	0;	Mismatches 325;	Indels 8;	Gaps 4

QY	72	CTGCAGGGCACTTCGGTCTGCTGGAGCTGTCCGGCCCTGGCCCCGGGCCCTTCTGTGCTATG	131
Db	2	CTGCGTGGCGCTCAGGGGTTCTTGAGACTTGCGAGGCCCTGGCCCCCAGGGCCGTTCTGCGGGATG	61
QY	132	GTCCCTGGCTGACTTCGGGGCGCGGTGTGCTACGCGGTGACCGCGGCCGCTCCCGTACGAC	191
Db	62	ATCCTGGCGGACTTCGGCGCCGAGGTGTGCTCTGTGACACAGACTGGGCTCCGTGAACCA	121
QY	192	GTGAGCCGCTTGGGGCCGGGGCAAGCGCTGCCTAGTGTCTGAGCTGAAGCAGCCGCGGGA	251
Db	122	CCCAGTCACTGGCCCGAGGCAAGCGCTGCTGGCGCTGAGCTGAAGCGGTCTCCGGGA	181
QY	252	GCCGCGGTGCTGCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGTGGAGCCCTCCGCCG	311
Db	182	GCCGCGGTGTGCGGGCGCATGTGCGCACGCGCGGACGTGTGCTGAGACCCCTCCGTTGC	241
QY	312	GGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCAAAGCTT	371
Db	242	GGTGTATGAGAAACTCCAGCTTGGGCCAGAGACTCTACGGCAGAGCAATCCAAAGCTC	301
QY	372	ATTATGCCAGCTGAGTGGATTGTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCAC	431
Db	302	ATCTATGCCAGCTGAGTGGATTGTGGCCAGTCGGGAATTTCTCCAAAGTAGCTGGCCAT	361
QY	432	GATATCAACTATTGGCTTTGTACAGGTCTCTCATAAAATTTGGCAGAAAGTGTGAGAA	491
Db	362	GACATCAACTATGTGGCTTTGTACAGGTCTCTGTCAAAAGATTGGCAGGAGCGTGAGAAC	421
QY	492	CCGTATGCCCGCTGAATCTCTGCGCTGACTTTGCTGTGTGGGACCTTATGTGACATG	551
Db	422	CCATACCCTCCCTGAACCTCCTGGCGACTTTGGTGGCGGTGGCCTCATGTGCACATTG	481
QY	552	GGCATTTAATGGCTCTTTTGCACCGACACACGCACCTGGCAAGGTCAGGTCATTGATGA	611
Db	482	GGCATTTTGTGGCTCTCTTTCGAACCGACCGCGGTCTGGCCTTAGGGCAAGGTCATTGATGCG	541
QY	612	AATATGGTGAAGGAACAGCATATTAAAGTCTTTCTGTGTGAAAACTCAGAAATCGAGT	671
Db	542	AACATGGTGAAGGAACGCGCATACTTAAAGTACTTTCCTGTGTGAAAACTCAGGCCATGGT	601
QY	672	CTGTGGGAAGCACTCGAGGACAGACATGTTGGATGTGAGCACTTTCCTATACGACT	731
Db	602	CTGTGGGACAGCCTCGAGGGCAAACTGTTAGATGGCGGGCACCTTCTTACACAAAC	661
QY	732	TACAGGACAGAGATGGGGAATTCAATGCTGTTGGAGCAATAGAACCCAGTTCTACGAG	791
Db	662	TACAAGACCGAGATGGGGAGTTCATGGCTGTAGTGCATATGAACCCAGTTCTACACA	721
QY	792	CTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCAATCAGATGAGCATGAT	851
Db	722	CTGCTGCTTAAAGGACTTGGACTTAAAGTCTGAGGAACCTCCCAAGCAGATGAGCATAGAA	781
QY	852	GATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTTGCCAAAGACGAAAGCGACGAG	911
Db	782	GATTGGCCAGAAATGAAGAAGAAATTTGCAGATGTGTTTGCAGGAAGAAAGACTTAAGCAGAG	841

OY	912	TGCTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCCTGACTTTTGAGAG	971
Db	842	TGGTGCAGATCTTTGACGGACAGATGCATGTGTGACCACCAGTGTGACTCTTGAGGAG	901
OY	972	GTTGTTCATCATGATCACAAGAAGAACGGGGCTCGTTTATCACCACTGAGGAGCAGGAC	1031
Db	902	GCCCTCCACCACACAGCACAAGAGAACGGGGCTCTCTTCATCACTGATGAGGAGCAGCAT	961
OY	1032	GTCAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATCCCTCTTTCAAAGG	1091
Db	962	GCATGCCCCCGCTCCTGCACCCACAGCTTTCAGAAACCCCTGCTGTCTCTGCCCCAAGG	1021
OY	1092	GATCCTTTCATAGGAGAGAACACACTGAGGAGATACTTGAAGAATTGGATTACGCCGGA	1151
Db	1022	GACCTTCTGTGGAGAGACACACTGTAGAGGTGCTTAAGACTATGGATTACGTGAGAA	1081
OY	1152	GAGATTTATCAGCTTAACTTCAGATAAAATCATTTGAAGTAATAAGGTAAGGCTAGTCTC	1211
Db	1082	GAGATTCATCAGCTGCACCTCGATGATAGAATCATTTGAAGTAATAAGCTAAAGGCCA	1141
OY	1212	TAACTTCCAGGCCACGGCTCAAGTGAATTTGAATPACTGCATTTACAGTGTAGAGTAACA	1271
Db	1142	TGACT--CAGGTTACAGCTCAAGTGAATCTGAAGCGCTATCTGTACTGAGAAAGATG	1199
OY	1272	CATAACATTGTATGCATGGAACATGGAGGAGACAGTAATTACAGTGTCTTACCACCTCTAAT	1331
Db	1200	CCCACCACCTGTCGATGGAATGTGAATGAACAGTAATGAAGTAATCCAATATTCCAA	1259
OY	1332	CAAGAAAAGAAATTACAGACTCTGATTTCTACAGTGAATGAATTTCAAAAAATGGTATC	1391
Db	1260	TCAAGACACAACGAAAAGA--CTGATTACAGAGAAATGACTGTGCTCTCACACTGCTCATC	1317
OY	1392	--ATTAGGGCTTTTGATTTATAAAACCTTTGGGTACTTATACTAAATTATGGTAGTATT	1448
Db	1318	CGAGCCTCTGATTTGAGAGATATTTTTGTGTGTACTATGATATTAACCTTGTGGCAGTT-TT	1376
OY	1449	CTGCCCTTCAGTTTGGCTTGATATATT	1474
Db	1377	CTGCCCTTTCAGCTTACTTGGTGAAGT	1402

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RESULT 12
US-10-301-856-852
; Sequence 852, Application US/10301856
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Nephrotoxicology Modeling
; FILE REFERENCE: 44921-5089-01
; CURRENT APPLICATION NUMBER: US/10/301, 856
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 10/152, 319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292, 335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297, 523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298, 925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303, 810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303, 807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303, 808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315, 047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324, 928

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: PRIOR FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: US 60/330,867
: PRIOR FILING DATE: 2001-11-01
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 1261
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 852
: LENGTH: 1504
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-301-856-852

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Query Match      41.4%; Score 830; DB 8; Length 1504;
Best Local Similarity 76.3%; Pred. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

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OY 72 CTGACGACATCTCGGTCTGTGAGAGCTGTCCGGCCCTGGCCCGGCGCCGTTCTGTGCTATG 131
DB 2 CTGCGTGGCGTCAAGGTTCTGTGAGAGCTGTGCGAGGCTTGCCCGGCGGCGTTCTGTGCGGATG 61
OY 132 GTCTGGCTGACTTCGGGGCGCGTGTGTGACCGGTGAGACCGCGCGCTCCGCTACGAC 191
DB 62 ATCTGGCGGACTTCGGCGCGGAGGTGTGTGCTGTGACAGACTGGGCTCCGTGAACAC 121
OY 192 GTGAGCCGCTGGGGCGGGGCAAGCGCTCGCTAGTGTGTGACCTGAAGCAGCGCGGGA 251
DB 122 CCCAGTCACTGCGCCCGAGGCAAGCGCTCGCTGCGCTGACCTGAAGCGGCTCCGGA 181
OY 252 GCCCGCGTGTGCGCGCTGTGTGCAAGCGGTGTGTGCTGTGAGCCCTCCGCGC 311
DB 182 GCCGCGGTGTGCGCGCGCATGTGCGCAGCGCGGAGCGTGTGTGTGAGCCCTCCGTTGC 241
OY 312 GGTGTGATGAGAAACTCCAGCTGGGGCCAGAGATTTCTGACCGGGAAATCCAGGCTT 371
DB 242 GGTGTGATGAGAAACTCCAGCTGGGGCCAGAGACTCTACGGCAGAGCAATCCAAAGCTC 301
OY 372 ATTTATGCCAGCTGAGTGTGAGTGTGCGCAGTCAAGAGCTTGTGCGGTGTGAGCGCCAC 431
DB 302 ATCTATGCCAGCTGAGTGTGAGTGTGCGCAGTCAAGAGCTTGTGCGGTGTGAGCGCCAT 361
OY 432 GATATCACTATTTGGCTTGTGTCAAGTGTGTCTCAAAAATTTGGCAGAGTGTGAGAT 491
DB 362 GACATCACTATTTGGCTTGTGTCAAGTGTGTCTCAAAAATTTGGCAGAGTGTGAGAT 421
OY 492 CCGTATGCCCGCTGATCTCTGCTGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
DB 422 CCATACCTCTCCCTGAACCTCTGCGCGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481
OY 552 GGCATTATATGCTCTTTTGTGACCGCAGCAGCAGCTGTGCAAGGCTCAGTCTATGATGA 611
DB 482 GGCATTATGCTCTCTCTGTGACCGCAGCAGCAGCTGTGCAAGGCTCAGTCTATGATGA 541
OY 612 AATATGTTGAAGGAACAGCATATTTAGTCTTTTCTGTGAGAAACTCAGAAATCGAGT 671
DB 542 AACATGTTGAAGGAACAGCATATTTAGTCTTTTCTGTGAGAAACTCAGAAATCGAGT 601
OY 672 CTGTGGGAAGCAGCTGTGAGGAGAAACATGTGTGAGTGTGTGAGCAGCTTTCTATACGACT 731
DB 602 CTGTGGGACAGCCTGTGAGGAGAAACCTGTGTGAGTGTGTGAGCAGCTTTCTATACAGCC 661
OY 732 TACAGGACAGAGATGGGAATTCATGGCTTTGTGAGCAATAGAACCCAGTTCTACGAG 791
DB 662 TACAAGACCGCAGATGGGAGTTCATGGCTGTAGGTGCAATAGAACCCAGTTCTACACA 721
OY 792 CTGCTGATCAAGGACTTGAAGTCTGATGAAGTCTCCCAATCAGATGAGCATGAT 851
DB 722 CTGCTGCTTAAAGGACTTGAAGTCTGAGGAAGTCTCCCAAGATGAGCATAGAA 781
OY 852 GATTGGCCAGAAATGAAGAGAGTTTGACAGATGTATTTGCAAGAGAGAGAGGACAGAG 911
DB 782 GATTGGCCAGAAATGAAGAGAGTTTGACAGATGTGTGCAAGAGAGAGACTTAAGGACAGAG 841

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OY 912 TGGTGTCAAAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTGTGACTTTTGAGAG 971
DB 842 TGGTGCCAGATCTTTGACGGGAGAGATGCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 901
OY 972 GTTGTTCATCATCATCACAACAAGAGAGAGCGGGCTCGTTTATCACCAGTGAAGAGAGAGAC 1031
DB 902 GCCCTCCAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
OY 1032 GTGAGCCCGCCCGCTGACAGCTGTGTGTGAAACAGCCCGCAGTCCCTTTTCAAAAG 1091
DB 962 GCATGCCCGCCCGCTGACAGCAGCTGTGTGAAACAGCCCGCAGTCCCTTTTCAAAAG 1021
OY 1092 GATCCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
DB 1022 GACCTTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
OY 1152 GAGATTTATCAGCTTAACTCAGATTAATAATCATTTGAAGTAAATGAAGTAAAGCTAGTCTC 1211
DB 1082 GAGATTCATCAGCTGTGACAGCTGAGATGAATCATTTGAAGTAAATGAAGTAAAGCTAGTCTC 1141
OY 1212 TAACTTCCAGAGCCAGCGCTCAAGTGAATTTGAATTTGATTTTACAGTGTAGAGTAAACA 1271
DB 1142 TGAAT--CAGTTTACAGCTCAAGTGAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1199
OY 1272 CATACATTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
DB 1200 CCCACCACTGTCCGTATGAATGTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259
OY 1332 CAAGAAAGAAATTTACAGACTGTGATTTTACAGTGTATGATTTCTAAATAATGTTATTC 1391
DB 1260 TCAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317
OY 1392 ---ATTAGGCTTTTGTATTTAAACTTTGGCTTACTTATTAATTAATTAATTAATTAAT 1448
DB 1318 CGAGCCTCTGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1376
OY 1449 CTGCTTTCAGCTTTGCTGTGATTAATTT 1474
DB 1377 CTGCTTTCAGCTTACTTGTGTAAGT 1402

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RESULT 13
US-10-338-044-1802
: Sequence 1802, Application Us/10338044
: GENERAL INFORMATION:
: APPLICANT: MENDRICK, Donna
: APPLICANT: PORTER, Mark
: APPLICANT: JOHNSON, Kory
: APPLICANT: HIGGS, Brandon
: APPLICANT: CASTLE, Arthur
: APPLICANT: ELASHOFF, Michael
: TITLE OF INVENTION: Molecular Cardiolotoxicology Modeling
: FILE REFERENCE: 44921-5090-01-US
: CURRENT APPLICATION NUMBER: US/10/338,044
: PRIOR FILING DATE: 2003-01-27
: PRIOR APPLICATION NUMBER: US 60/303,819
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/305,623
: PRIOR FILING DATE: 2001-07-17
: PRIOR APPLICATION NUMBER: US 60/369,351
: PRIOR FILING DATE: 2002-04-03
: PRIOR APPLICATION NUMBER: US 60/377,611
: PRIOR FILING DATE: 2002-05-06
: NUMBER OF SEQ ID NOS: 2696
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1802
: LENGTH: 1504
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. NM_012816
US-10-338-044-1802

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Query Match	41.4%;	Score 830;	DB 8;	Length 1504;
Best Local Similarity	76.3%;	Pred. No. 2e-195;		
Matches 1073; Conservative	0;	Mismatches 325;	Indels 8;	Gaps 4;

QY	72	CTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCCTGGCCCCGGGCCGTTCTGTGCTATG	131
Db	2	CTGCGTGGCGTCAGGGTCTTGGAGCTGGCAGGCCCTGGCCCCAGGGGCCGTTCTGCGGGATG	61
QY	132	GTCCCTGGCTGACTTCGGGCGCGCTGTGTGACGCGTGAACCGGCGCCGCTCCGCTACGAC	191
Db	62	ATCTGGCGGACTTCGGGCGCCGAGGTGTGTCTGTGACAGACTGGGCTCCGTGAACCA	121
QY	192	GTGAGCCGCTTGGGCGCGGCGCAAGCGCTGCTAGTGTGTGACCTGAAGCAGCGCGGGGA	251
Db	122	CCCAGTCACTGTGCCCGGAGGCAAGCGCTGCTGGCGCTGGAACCTGAAGCGGTCTCCGGGA	181
QY	252	GCCGCGCTGTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGTGAGCCCTCCGCGC	311
Db	182	GCCGCGGTGTGCGGCGCATGTGCCGACGCGCGGACGCTGTGCTGAGCCCTTCCGTTGC	241
QY	312	GGTGTCAATGAGAACTCCACGCTGGGCCAGAGATTCTGACGCGGGAATCCAAAGCTT	371
Db	242	GGTGTCAATGAGAACTCCACGCTTGGGCCAGAGACTCTACGGCAGGACAAATCCAAAGCTC	301
QY	372	ATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCAC	431
Db	302	ATCTATGCCAGGCTGAGTGGATTTGGCCAGTCGGGAATTTCTCCAAGTAGCTGGCCAT	361
QY	432	GATATCAACTATTTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAAGTGTGAGAT	491
Db	362	GACATCAACTATGTGGCTTTGTCAAGGTGTCCTGTCAAAAGATTGGCAGGCGGTGAGAAC	421
QY	492	CCGTATGCCCCGCTGAATCTCCTGGCTGACCTTGTGCTGGCTGGCCCTTATGTGTGACATG	551
Db	422	CCATACCCCTCCCTGAACCTCCTGGCCGACTTGTGTGGCGGTGGCCCTCATGTGCACATTG	481
QY	552	GGCATTATATAGGCTCTTTTGAACCGCACACGACCTGGCAAGGGTCAAGTCAATTGATGCA	611
Db	482	GGCATTTTGTGCTGCTCTCTGAAACGCACGCGGTCTGGCTAAGGCAAGTCAATTGATGCG	541
QY	612	AATATGTTGAAGAAACAGCATATTTAAGTCTTTCTGTGGAAAACTCAGAATCGAGT	671
Db	542	AACATGTTGAAGAAACGCGCATACTTAAGTACTTTCCTGTGGAAAACTCAGGCCATGGGT	601
QY	672	CTGTGGGAAGCACCTCGAGCAGACAGAACATGTTGATGTTGAGACACACTTCTATACGACT	731
Db	602	CTGTGGGACACAGCCTCGAGGCGCAAAACCTGTTAGATGGCGGGGACACTTCTACACAAAC	661
QY	732	TACAGGACAGCAGATGGGGAATTCATGCGTGTGGAGCAATGAACCCAGTTCACGAG	791
Db	662	TACAAGACCGCAGATGGGAGTTCATGGCTGTAGGTGCAATGAACCCAGTTCACACA	721
QY	792	CTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGAT	851
Db	722	CTGCTGCTTAAAGGACTTGGACTTGAAGTCTGAGGAACCTCCACGACATGAGCATAGAA	781
QY	852	GATTGGCCAGAAATGAAGAAGATTGTGAGATGTATTGCAAAAGAAAGACGAAGGCAGAG	911
Db	782	GATTGGCCAGAAATGAAGAAGAAATTTGAGATGTGTTGCAAGGAAGACTAAGGCAGAG	841
QY	912	TGCTGTCAAAATCTTTGAGCGCACAGATGCGTGTGACTCCGGTTCTGACTTTTGAGGAG	971
Db	842	TGCTGTCAAAATCTTTGAGCGGACAGATGCTGTGACCCCACTGCTGACTCTTGAGGAG	901
QY	972	GTTGTTCATCATGATCACAACAAGAAACGGGGCTGTTTACACAGTGAGGACAGGAC	1031
Db	902	GCCCTCCACCAACCAAGCACACAAGAAACGGGGCTCCTTCACTCATGATGAGGACAGCAT	961
QY	1032	GTTGAGCCCCCGGCTGCACTCTGCTGTTAAACACCCCAAGCATCCCTTCTTCAAAAGG	1091
Db	962	GCAATGCCCCGCTCTGCAACCCAGCTTTCAGAAACCCCTGCTGTCTTCTGCCCCAAAGG	1021

QY	1092	GATCCCTTTTCATAGGAGAACACACTGAGGAGATACCTGAAGAAATTTGGATTCAGCCGGAA	1151
Db	1022	GACCCCTTCTGTGGAGAGCACACTGTAGAGGTGCTTAAAGACTATGGATTCACTCAGGAA	1081
QY	1152	GAGATTTCAGCTTAACTCAGATAAATCATTTGAAAGTAATAAGGTAAGCAAGCTACTC	1211
Db	1082	GAGATCCATCAGCTGCACCTCGATAGATGAAATCATTTGAAGTAATAAGCTAAAAGCCAACTC	1141
QY	1212	TAACTTCCAGGCCACGGCTCAAGTGAATTTGAATCTGCATTTACAGTGTAGATAACA	1271
Db	1142	TGACT--CAGGTTACACAGCTCAAGTGAATCTGAAGGCTGTATCTGTACTGGAGAGGATG	1199
QY	1272	CATAACATTTGTATGCATGGAACATGGAGGAACAGTATTACAGTGTCCACACTCTAAT	1331
Db	1200	CCCACCACCTGTCCGTATGGAATGTGAATGAACAGTATGAAGTAATCCAAATATCCAA	1259
QY	1332	CAAGAAAGAATTTACAGACTCTGATTTCTACAGTGATGATTTGAATTCCTAAAAATGGTTATC	1391
Db	1260	TCAAGACACACAACGAAGA--CTGATTACAGAGAAATGACTGTGCTCTCACACTGCTCATC	1317
QY	1392	---ATTAGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAAATATATGGTACTTAT	1448
Db	1318	CGAGCCTCTGATTGAGGAGTATTTTGTGTGTGTACTGATATTAACTTGTGGCAGTT--TT	1376
QY	1449	CTGCCCTTCCAGTTTGCTTGATATATT	1474
Db	1377	CTGCCCTTTCAGCTTACTGTGTTGAAGT	1402

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RESULT 14
US-10-256-909-172
; Sequence 172, Application US/10256909
; GENERAL INFORMATION:
; APPLICANT: Bader, Joel S.
; APPLICANT: Czar, Michael J.
; APPLICANT: Decristofaro, Marc F.
; APPLICANT: Gerwien, Robert W.
; APPLICANT: Hershman, Kenneth M.
; APPLICANT: Lakkis, Maha
; APPLICANT: Mansfield, Traci A.
; APPLICANT: McCabe, Denise
; APPLICANT: Olsen, H19h
; TITLE OF INVENTION: CHOLESTASIS- ASSOCIATED MARKERS AND METHOD OF USE THEREOF
; FILE REFERENCE: 21402-458
; CURRENT APPLICATION NUMBER: US/10/256, 909
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/325, 609
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 172
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-256-909-172

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Query Match	41.4%	Score 830	DB 8	Length 1504
Best Local Similarity	76.3%	Pred. No. 2e-195		
Matches 1073	Conservative 0	Mismatches 325	Indels 8	Gaps 4
QY	72	CTGCAGGGCATCTCGTCTGAGACTGTCCGGCCTGGCCCCCGGCGTTCTGTGTATG	131	
Db	2	CTGCCTGGCGCTCAGGGTTCTGGACCTGGCAGGCCCTGGCCCCCAGGGCGCTTCTGCGGGATG	61	
QY	132	GTCCTGGCTGACTTCGGGGCGCGCTGTGTGTACGGCTGGACCGCGCCCGGCTCCCGCTACGAC	191	
Db	62	ATCCTGGCGACTTCGGCGCCGAGGTGTGTCTCTGTGGACAGACTGGGGCTCCGTGAACCCAC	121	
QY	192	GTGAGCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGTGACCTGAAGCAGCGCGGGGA	251	
Db	122	CCCACTCACCCTGGCCCCGAGGCAAGCGCTCGCTGGCGCTGGACCTGAAGCGGTCTCCGGGA	181	
QY	252	GCCGCGGTGCTGCGGGCTCTGTGCAAGCGGTGGATGTGCTGTGAGAGCCCTTCGCGCCG	311	

Db 182 GCCGCGGTGTGGCGGCATGTGGCACGCGCGGACGTTGTGTGAGAGCCCTTCGTTGC 241
QY 312 GGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATAATCCAGGCTT 371
Db 242 GGTGTCATGAGAACTCCAGCTGGGCCAGAGACTCTACGGCAGACAATCCAAAGCTC 301
QY 372 ATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGAGAGCTTCTGCCGGTTAGCTGCCAC 431
Db 302 ATCTATGCCAGGCTGAGTGGATTGGCCAGTCGGGAATTTCTCCAAGTAGCTGGCCAT 361
QY 432 GATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAGAGTGGTAGAAT 491
Db 362 GACATCAACTATGTGCTTTGTGAGTGTCTCTCAAAAAGATTGGCAGCGGTGAGAAC 421
QY 492 CCGTATGCCCGCTGAATCTCCGTGCTGACTTTGCTGGTGGTGGCTTATGTGCACTG 551
Db 422 CCAATACCTCCCTGAACCTCCTGCGGCACTTTGGTGGCGGTGCTCATGTGCACATTG 481
QY 552 GGCATTATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTGATGCA 611
Db 482 GGCATTTTGTGCTGCTCTCTTGAACGCACGCGGTGGCCTAGGGCAGGTGATGTGCG 541
QY 612 AATATGGTGAAGGACAGCATATTTAAGTTCTTTCTGTGAAAACTCAGAAATGAGT 671
Db 542 AACATGGTGAAGGACCGCATACTTAAGTACTTCTGTGAAAACTCAGGCCATGGGT 601
QY 672 CTGTGGGAAGCACCCTCGAGGACAGACATGTGTGATGTTGGAGCACCTTCTATACGACT 731
Db 602 CTGTGGGCACAGCCTCGAGGGCAAACTGTTAGATGGCGGGCACTTCTACACAAC 661
QY 732 TACAGGACAGACAGATGGGGAATTGCTGTGTGAGCAATAGAACCCAGTCTPACGAG 791
Db 662 TACAAGACCGCAGATGGGGAGTTCATGGCTGTAGTGCAATAGAACCCAGTTCTACACA 721
QY 792 CTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGAT 851
Db 722 CTGCTGCTTAAGAGACTTGGACTGTGAGTCTGAGGAATCCCAAGCAGATGAGCATAGAA 781
QY 852 GATTGGCCAGAAATGAAGAAGTTTGACAGATGTATTGCAAGAAGACGAAGCGAGAG 911
Db 782 GATTGGCCAGAAATGAAGAAGTTTGACAGATGTATTGCAAGAAGACTAAGCGAGAG 841
QY 912 TGTGTCAAAATCTTTGACGGGCACAGATGCCGTGTGACTCCGGTCTGACTTTGAGGAG 971
Db 842 TGTGTCCAGATCTTTGACGGGACAGATGATGTGTGACCCCAAGTGTGACTCTTGAGGAG 901
QY 972 GTTGTTCATCATGATCACACAAGAAGCGGGCTTTATCACCACTGAGAGCGAGAC 1031
Db 902 GCCCTCCACACACACACAAGAAGCGGGCTCTTCATCATGATGAGAGCGAGCAT 961
QY 1032 GTGAGCCCCCGCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAAG 1091
Db 962 GCATGCCCCCGTCTGTGCACCCCAAGCTTTCAGAACCCCTGTCTCTTGTGCCAAAAG 1021
QY 1092 GATCCTTTCATAGAGAAACACACTGAGGAGATGATGAAAGATTGATTGAGTCAGCGGAA 1151
Db 1022 GACCTTCTGTGGAGAGACACACTGTAGAGGTCTTAAAGACTATGGAATTCAGTCAGGAA 1081
QY 1152 GAGATTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAGCTAAAGCTPACTCTC 1211
Db 1082 GAGATCCATCAGCTGACACTCGAATGAATCATGTGAAGTAATAGCTAAAGCCAACTC 1141
QY 1212 TAACTTCCAGGCCCAAGGCTCAAGTGAATTGAACTGCAATTTACAGTGTAGATAACA 1271
Db 1142 TGAAT--CAGGTTCAAGCTCAAGTGAATCTGAAGCTGTATCTGTAAGAGAGATG 1199
QY 1272 CATTAACATTGTATGATGAAACATGAGAGACAGTATTACAGTGTCTTACCACCTTAAT 1331
Db 1200 CCCACCACTGTCCGATATGAAATGGAATGAACAGTAATGAAGTAATCCAAATATTCCAA 1259
QY 1332 CAAGAAAAGAATTCAGACTCTGATTTCTACAGTGAATGATTGAATTTAAATGTTATC 1391

Db 1260 TCAAGACACAACGAAGA--CTGATTACAGAGAAATGACTGTGCTCTCACACTGCTCATC 1317
QY 1392 --ATTAGGCTTTGATTATATAAACTTTGGGTACTTATACTAAATTATGTAATT 1448
Db 1318 CGAGCCTCTGATTGAGAGATATTTTGTGTGTACTGATATTAATCTGTGGCAGTT-TT 1376
QY 1449 CTGCTTCCAGTTTCTGATATATT 1474
Db 1377 CTGCTTTCAGCTTACTTGTGTAAGT 1402

RESULT 15
US-60-436-643-3149
; Sequence 3149, Application US/60436643
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castie, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-P15
; CURRENT APPLICATION NUMBER: US/60/436,643
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; PRIOR FILING DATE: 2001-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4295
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3149
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012816
US-60-436-643-3149

Query Match 41.4%; Score 830; DB 9; Length 1504;
Best Local Similarity 76.3%; Pred. No. 2e-195;
Matches 1073; Conservative 0; Mismatches 325; Indels 8; Gaps 4;

QY 72 CTGACGGCATCTGCGTGTGAGCTGTCCGGGCTGGCCCCGGCCGCTTCTGTGCTATG 131
Db 2 CTGCGTGGCGTCAAGGTTCTGTGAGCTGGCAGGCGCTGGCCCCCAGGCGCTTCTGCGGATG 61
QY 132 GTCTGCGCTGACTTGGGGCGCGGTGTGTACGCGTGGACCGGCGCGCTCCCGCTACGAC 191
Db 62 ATCTGCGGAGCTTGGCGCGCGAGGTGTGCTGCTGTGACAGACTGGGCTCCGTTGAACAC 121
QY 192 GTGACCGGCTTGGCGCGGGCAAGCGCTGCTAGTGTGACCTGAAGCAGCGCGGGGA 251
Db 122 CCCAGTCACCTGGCGCGGAGCAAGCGCTGCTGGCGCTGAGCTGAAGCGGCTTCCGGGA 181
QY 252 GCCGCGGTGCTGCGGCGTCTGTGCAAGCGGTCGATGTGTGTGAGACCCCTTCCGCGCG 311

Db 182 GCCCGGTGTGCGGCATGTGCGCACGCGGACGTGTGCTGGAGCCCTTCCGTGTC 241
QY 312 GGTTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGCTT 371
Db 242 GGTGCATGGAGAACTCCAGCTGGGCCAGAGACTCTACGGCAGACAATCCAAAGCTC 301
QY 372 ATTTATGCCAGCTGAGTGAATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCAC 431
Db 302 ATCTATGCCAGGCTGAGTGGATTGGCCAGTCGGGAATTTCTCCAAAGTAGCTGGCCAT 361
QY 432 GATATCAACTATTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAAAGTGGTAGAAT 491
Db 362 GACATCAACTATGTGGCTTTGTCAAGGTGTCTCTCAAAAGATTGGCAGGAGCGGTGAGAAC 421
QY 492 CCGTATGCCCCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCCTTATGTGCACTG 551
Db 422 CCATACCTTCCCTGAACCTCTGGCCGACTTGTGGTGGCGCTCATGTGCACATTG 481
QY 552 GGCATTATTAATGGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGTCAATTGATGA 611
Db 482 GGCATTTTGCTGGCTCTCTTCGAACGCACGCGTCTGGCCTAGGGCAGTCAATTGATGCG 541
QY 612 AATATGCTGGAAGGAACAGCAATATTAAATTCTTTCTGTGGAATACTCAGAAATCGAGT 671
Db 542 AACATGCTGGAAGGAACGCAATCTTAAGTACTTCTGTGGAATACTCAGGCCATGGGT 601
QY 672 CTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGGTGGAGCACCTTCTATACGACT 731
Db 602 CTGTGGGCACAGCCTCGAGGGCAAAACCTGTTAGATGGCGGGGCACCTTCTACACAACC 661
QY 732 TACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTCTACGAG 791
Db 662 TACAAGACCCGACAGATGGGAGTTCAATGGCTGTAGGTGCAATAGAACCCAGTCTACACA 721
QY 792 CTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGAT 851
Db 722 CTGCTGCTTAAAGGACTTGGACTTGAAGTCTGAGGAACCTCCCAAGCATGAGCATAGAA 781
QY 852 GATTGGCCAGAAATGAAGAAGATTGGCAGATGTATTGGCAAGAAGAGGAGGAGAG 911
Db 782 GATTGGCCAGAAATGAAGAAGAAATTTGCAGATGTGTTGCAAGGAAGACTAAGGCAGAG 841
QY 912 TGGTGTCAAACTTTGACGGCACAGATGCCGTGTGACTCCGCTTCTGACTTTTGAGGAG 971
Db 842 TGGTGGCAGATCTTTGACGGGACAGATGATGTGACCCCAAGTGTGACTCTTGAGGAG 901
QY 972 GTTGTTCATCATGATCACAACAAGAAAGGGGCTCGTTTATCACCAAGTGAGAGCAGAC 1031
Db 902 GCCCTCCACACACAGCACACAAGAAAGGGGCTCCTTCATCACATGATGAGAGCAGCAT 961
QY 1032 GTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCCAAGCATCCCTTCTTCAAAAG 1091
Db 962 GCATGCCCCCGTCTCTGCACCCCAAGCTTTCAGAAACCCCTGCTTCTTGCCAAAAG 1021
QY 1092 GATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTCAAGCCCGAA 1151
Db 1022 GACCTTCTGTGGAGAGACACTGTAGAGGTCTTAAAGACTATGGATTCACTCAGGAA 1081
QY 1152 GAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAGGTAAGGTAAGCTAGTCTC 1211
Db 1082 GAGATTCATCAGCTGCACCTGGATGAATCATTTGAAAGTAATAGCTTAAAGCCAACTCTC 1141
QY 1212 TAACTTCCAGGCCACGCTCAAGTGAATTTGAATTAATGATCTTACAGTGTAGAGTAACA 1271
Db 1142 TGAAT--CAGGTTACAGAGCTCAAGTGAATCTGAAGGCTGTATCTGTACTGAGAAAGATG 1199
QY 1272 CATTAACATTGTATGATGAAGAAATGAGAGAACAGATATTACAGTGTCTACCACTCTAAT 1331
Db 1200 CCCACCACTGTCCGTATGGAATGTGAATGAACAGTAATGAATCAATATATTCCAA 1259
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Db 1260 TCAAGACACAACGAAGA--CTGATTACAGAGAAATGACTGTGCTCTCACACTGCTCATC 1317
QY 1392 ---ATTAGGCTTTTGATTTATAAAACTTTGGTACTTATTAATTAATGATGTTATT 1448
Db 1318 CGAGCCTCTGATGAGGAGATATTTTGTGTGTACTGATATTAATTAATTTGTCGACGTT-TT 1376
QY 1449 CTGCCCTCCAGTTTGTGCTGATATATT 1474
Db 1377 CTGCCCTTCAGCTTACTTGTGAAGT 1402

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Job time : 718.574 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2003, 21:40:44 ; Search time 188.983 Seconds
(without alignments)
9306.248 Million cell updates/sec

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Perfect score:	2005
Sequence:	1 ttgaagctgctgctgg.....acatccagaataaagtct 2005

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

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Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2005	100.0	2005	10	US-09-967-305-1	Sequence 1, Appl
2	2003.4	99.9	2005	10	US-09-967-305-10	Sequence 10, App
3	2003.4	99.9	2069	10	US-09-967-305-4	Sequence 4, Appl
4	1671.4	83.4	3023	10	US-09-967-305-8	Sequence 8, Appl
5	1574.2	78.5	1621	9	US-09-232-880-107	Sequence 107, App
6	1574.2	78.5	1621	9	US-10-012-896-107	Sequence 107, App
7	1574.2	78.5	1621	9	US-09-895-793-107	Sequence 107, App
8	1574.2	78.5	1621	9	US-09-895-814-107	Sequence 107, App
9	1574.2	78.5	1621	10	US-09-759-143-107	Sequence 107, App
10	1574.2	78.5	1621	10	US-09-780-669-107	Sequence 107, App
11	1574.2	78.5	1621	10	US-09-030-606-107	Sequence 107, App
12	1574.2	78.5	1621	10	US-09-822-827-107	Sequence 107, App
13	1574.2	78.5	1621	10	US-09-115-453-107	Sequence 107, App
14	1197	59.7	3654	10	US-09-967-305-6	Sequence 6, Appl
15	1146	57.2	1146	10	US-09-967-305-3	Sequence 3, Appl
16	830	41.4	1504	10	US-09-917-800A-1576	Sequence 1576, App
17	515	25.7	537	9	US-09-232-880-74	Sequence 74, Appl
18	515	25.7	537	9	US-10-012-896-74	Sequence 74, Appl
19	515	25.7	537	9	US-09-895-793-74	Sequence 74, Appl

ALIGNMENTS

20	515	25.7	537	9	US-09-895-814-74	Sequence 74, Appl
21	515	25.7	537	10	US-09-759-143-74	Sequence 74, Appl
22	515	25.7	537	10	US-09-780-669-74	Sequence 74, Appl
23	515	25.7	537	10	US-09-030-606-74	Sequence 74, Appl
24	515	25.7	537	10	US-09-822-827-74	Sequence 74, Appl
25	515	25.7	537	10	US-09-115-453-74	Sequence 74, Appl
26	442	22.0	526	10	US-09-864-761-12333	Sequence 12333, A
27	428.4	21.4	430	9	US-09-736-457-1504	Sequence 1504, Ap
28	428.4	21.4	430	9	US-09-902-941-1504	Sequence 1504, Ap
29	428.4	21.4	430	9	US-09-849-626-1504	Sequence 1504, Ap
30	428.4	21.4	430	9	US-10-017-754-1504	Sequence 1504, Ap
31	410.8	20.5	578	10	US-09-925-300-23	Sequence 23, Appl
32	406.6	20.3	773	9	US-09-232-880-3	Sequence 3, Appl1
33	406.6	20.3	773	9	US-10-012-896-3	Sequence 3, Appl1
34	406.6	20.3	773	9	US-09-895-793-3	Sequence 3, Appl1
35	406.6	20.3	773	9	US-09-895-814-3	Sequence 3, Appl1
36	406.6	20.3	773	10	US-09-759-143-3	Sequence 3, Appl1
37	406.6	20.3	773	10	US-09-780-669-3	Sequence 3, Appl1
38	406.6	20.3	773	10	US-09-030-606-3	Sequence 3, Appl1
39	406.6	20.3	773	10	US-09-822-827-3	Sequence 3, Appl1
40	406.6	20.3	773	10	US-09-115-453-3	Sequence 3, Appl1
41	403.2	20.1	793	9	US-09-232-880-33	Sequence 33, Appl
42	403.2	20.1	793	9	US-10-012-896-33	Sequence 33, Appl
43	403.2	20.1	793	9	US-09-895-793-33	Sequence 33, Appl
44	403.2	20.1	793	9	US-09-895-814-33	Sequence 33, Appl
45	403.2	20.1	793	10	US-09-759-143-33	Sequence 33, Appl

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RESULT 1
US-09-967-305-1
: Sequence 1, Application US/09967305
: Patent No. US20020123081A1
: GENERAL INFORMATION:
: APPLICANT: Richardson, Jennifer
: APPLICANT: Monahan, John
: TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
: TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
: FILE REFERENCE: 07334-312001
: CURRENT APPLICATION NUMBER: US/09/967,305
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US 60/236,238
: PRIOR FILING DATE: 2000-09-28
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 2005
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-967-305-1

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Query Match	100.0%;	Score 2005;	DB 10;	length 2005;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2005; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY 1	TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCACTTTCCCTTACAGGGGGACATGGGAA	60		
Db 1	TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCACTTTCCCTTACAGGGGGACACTGGGAA	60		
QY 61	GGGCCATGGCACTGCGACAGGGCATCTCGGTCGTGAGACTGTCCGGCCCTGGCCCCGGCCCGT	120		
Db 61	GGGCCATGGCACTGCGACAGGGCATCTCGGTCGTGAGACTGTCCGGCCCTGGCCCCGGCCCGT	120		
QY 121	TCTGTGCTATAGTTCCTGGCTGACTTTCGGGGCGCGTGTGCTACGCGTGGAACCGGGCCGGCT	180		
Db 121	TCTGTGCTATAGTTCCTGGCTGACTTTCGGGGCGCGTGTGCTACGCGTGGAACCGGGCCGGCT	180		
QY 181	CCCGCTACGAGCTGAGCCGCTTGGGCGCGGGCAAGCGCTCGCTAGTGCTTGACCTGAAGC	240		
Db 181	CCCGCTACGAGCTGAGCCGCTTGGGCGCGGGCAAGCGCTCGCTAGTGCTTGACCTGAAGC	240		

OY 241 AGCCGGGGAGCCGCCGTGCTGCGGCTCTGTGCAAGCGGTCCGATGTGCTGCTGAGC 300
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Db 241 AGCCGGGGAGCCGCCGTGCTGCGGCTCTGTGCAAGCGGTCCGATGTGCTGCTGAGC 300
OY 301 CCTTCCGGCGGGTGTATGGAGAAACTCCAGCTGGGCCAGAGATTTCTGCAGCGGGAAA 360
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Db 301 CCTTCCGGCGGGTGTATGGAGAAACTCCAGCTGGGCCAGAGATTTCTGCAGCGGGAAA 360
OY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCCGT 420
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Db 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCCGT 420
OY 421 TAGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTCTCTCAAAAAATTTGGCAGAA 480
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Db 421 TAGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTCTCTCAAAAAATTTGGCAGAA 480
OY 481 GTGGTGAGATCCGTATGCCCGGCTGAATCTCCGTGCTGACTTTGCTGTGTGGCCTTA 540
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Db 481 GTGGTGAGATCCGTATGCCCGGCTGAATCTCCGTGCTGACTTTGCTGTGTGGCCTTA 540
OY 541 TGTGTGCACTGGGCAATTAATGGCTCTTTTGTACCCGACACGCACTGGCAAGGCTCAGG 600
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Db 541 TGTGTGCACTGGGCAATTAATGGCTCTTTTGTACCCGACACGCACTGGCAAGGCTCAGG 600
OY 601 TCATTGATGCAAAATATGCTGGAAGAACAGCAGATATTTAAGTCTTTTCTGTGAAAACTC 660
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Db 601 TCATTGATGCAAAATATGCTGGAAGAACAGCAGATATTTAAGTCTTTTCTGTGAAAACTC 660
OY 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGCAGACAGATGTTGGATGTTGAGCACCCTT 720
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Db 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGCAGACAGATGTTGGATGTTGAGCACCCTT 720
OY 721 TCTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGAGCAATAGAACCC 780
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Db 721 TCTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGAGCAATAGAACCC 780
OY 781 AGTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAATCAGA 840
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Db 781 AGTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCAATCAGA 840
OY 841 TGAGCATGATGATGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGA 900
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Db 841 TGAGCATGATGATGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGA 900
OY 901 CGAAGGCAAGTGTGTCAAAATCTTTGACGGCAGAGATGCTGTGACTCCGGTCTGA 960
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OY 961 CTTTGTAGGAGTGTTCATCATGATCACAACAAGAACGGGCTCGTTATCACCACTG 1020
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Db 961 CTTTGTAGGAGTGTTCATCATGATCACAACAAGAACGGGCTCGTTATCACCACTG 1020
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OY 1081 CTTTCAAAAGGATCCTTTATAGAGAACACACTGAGAGATACTTGAAGATTGGAT 1140
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Db 1081 CTTTCAAAAGGATCCTTTATAGAGAACACACTGAGAGATACTTGAAGATTGGAT 1140
OY 1141 TCAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAAGGTAA 1200
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Db 1141 TCAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAAAGGTAA 1200
OY 1201 AAGCTAGTCTTAACCTTCAGGCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGT 1260
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Db 1201 AAGCTAGTCTTAACCTTCAGGCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGT 1260
OY 1261 GTAGAGTAACACATATCATTTGATGATGGAACATGAGGAACAGATATTACAGTGTCT 1320
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Db 1261 GTAGAGTAACACATATCATTTGATGATGGAACATGAGGAACAGATATTACAGTGTCT 1320
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OY 1381 AAATGTTATCATTAAGGCTTTTGTATTTATAAACTTTGGTACTTAATAATTATGG 1440
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Db 1441 TAGTTATTTCCCTTCCAGTTTGTGATATATTTGTGATATTAAGATTTCTGACTTAT 1500
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Db 1501 ATTTTGAATGGTCTTAGTGAAAAAGGAATGATATATTTCTGAAGACATCATATACATT 1560
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Db 1561 TATTTACACTCTTGTATTTCAATGTAGAAAAATGAGAAATGCCACAATTTGATGTGA 1620
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Db 1621 TAAAGTCAACGTGAACAGAGATGATTTGGTTCATCCAGGCCCTTTGTGCTGTGTCATG 1680
OY 1681 ATCTCCCTCTAAGCAGATTTCCAAACTTTAGCAACAGTTATCACACTTTGTATTTGCAAA 1740
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Db 1681 ATCTCCCTCTAAGCAGATTTCCAAACTTTAGCAACAGTTATCACACTTTGTATTTGCAAA 1740
OY 1741 GAAAAGTTTCACTCTGATTTGAATCAGATGCTTCAACTGAAAAAACAATATCCAAATA 1800
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Db 1741 GAAAAGTTTCACTCTGATTTGAATCAGATGCTTCAACTGAAAAAACAATATCCAAATA 1800
OY 1801 ATGAGGAATGTGTGGCTCAGTACGTAGAGTCAGAGGAGACAGTCAAGTTTAGGGTTGC 1860
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Db 1801 ATGAGGAATGTGTGGCTCAGTACGTAGAGTCAGAGGAGACAGTCAAGTTTAGGGTTGC 1860
OY 1861 CTGTATCCAGTAATCTGGGGCTGTTTCCCGTGGGCTCTGTGGGCTGTGACCTTTCCTT 1920
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Db 1861 CTGTATCCAGTAATCTGGGGCTGTTTCCCGTGGGCTCTGTGGGCTGTGACCTTTCCTT 1920
OY 1921 CTCATGTGTTGATTTCTCTCCAGGCTGTGAGCAAGTTCTGATCTTATACCAACACA 1980
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Db 1921 CTCATGTGTTGATTTCTCTCCAGGCTGTGAGCAAGTTCTGATCTTATACCAACACA 1980
OY 1981 CAGCAACATCCAGAAATAAAGTTCT 2005
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Db 1981 CAGCAACATCCAGAAATAAAGTTCT 2005

RESULT 2
US-09-967-305-10
; Sequence 10, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

Query Match									
Best Local Similarity 99.98; Score 2003.4; DB 10; Length 2005;									
Matches 2004; Conservative 100.0%; Pred. No. 0;									
0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	TTGCAGGCTGTGGGCTGGGGCTAAGGCTGCTCAGTTCTTCAGCGGGGCACTGGGAA	60						
Db	1	TTGCAGGCTGTGGGCTGGGGCTAAGGCTGCTCAGTTCTTCAGCGGGGCACTGGGAA	60						
QY	61	GGCCATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGCCGT	120						
Db	61	GGCCATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGCCGT	120						
QY	121	TCTGTCTATGCTCTGCTGCTGACTTTCGGGGCGGCTGTGTACGGCTGGACCGGGCGCT	180						
Db	121	TCTGTCTATGCTCTGCTGCTGACTTTCGGGGCGGCTGTGTACGGCTGGACCGGGCGCT	180						
QY	181	CCCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCCGCTCGTAACTGTGCTGAGCTGAAGC	240						
Db	181	CCCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCCGCTCGTAACTGTGCTGAGCTGAAGC	240						
QY	241	AGCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGC	300						
Db	241	AGCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGC	300						
QY	301	CCTTCCGCGCGGGTGTCAATGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGCAGCGGGAAA	360						
Db	301	CCTTCCGCGCGGGTGTCAATGAGAAACTCCAGCTGGGCCCCAGAGATTTCTGCAGCGGGAAA	360						
QY	361	ATCCAAGGCTTATTTATGCAAGCTGAGTGAATTTGGCCAGTCAAGAACTTCGTCGCCGT	420						
Db	361	ATCCAAGGCTTATTTATGCAAGCTGAGTGAATTTGGCCAGTCAAGAACTTCGTCGCCGT	420						
QY	421	TAGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTCTCTCAAAAATTGGCAGAA	480						
Db	421	TAGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTCTCTCAAAAATTGGCAGAA	480						
QY	481	GTGTGAGAAATCCGTATGCCCGCTGAATCTCCGCTGACTTTGCTGTGTGGCCCTTA	540						
Db	481	GTGTGAGAAATCCGTATGCCCGCTGAATCTCCGCTGACTTTGCTGTGTGGCCCTTA	540						
QY	541	TGTGTGCACTGGGCACTTATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGG	600						
Db	541	TGTGTGCACTGGGCACTTATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGG	600						
QY	601	TCATTGATGCAAAATATGTTGGAAGAACAGACATATTTAAGTCTTTCTGTGAAAACTC	660						
Db	601	TCATTGATGCAAAATATGTTGGAAGAACAGACATATTTAAGTCTTTCTGTGAAAACTC	660						
QY	661	AGAAATCGAGTCTGTGGGAAGCACTCGAAGGACAGAAATGTTGGATGGTGAAGCACTT	720						
Db	661	AGAAATCGAGTCTGTGGGAAGCACTCGAAGGACAGAAATGTTGGATGGTGAAGCACTT	720						
QY	721	TCTATACGACTTACAGGACAGATGGGGAATTCATGGCTTTGGAGCAATGAACCCC	780						
Db	721	TCTATACGACTTACAGGACAGATGGGGAATTCATGGCTTTGGAGCAATGAACCCC	780						
QY	781	AGTTCTACGACTGCTGATCAAAAGGACTTGAAGTCTGATGAACCTTCCCAATCAGA	840						
Db	781	AGTTCTACGACTGCTGATCAAAAGGACTTGAAGTCTGATGAACCTTCCCAATCAGA	840						
QY	841	TGAGCATGATGATTGGCCAGAAATGAAGAAGATTGACAGATGATTGCAAAAGAGA	900						
Db	841	TGAGCATGATGATTGGCCAGAAATGAAGAAGATTGACAGATGATTGCAAAAGAGA	900						
QY	901	CGAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGTGACTCCGGTCTGA	960						
Db	901	CGAAGGACAGTGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGTGACTCCGGTCTGA	960						
QY	961	CTTTTGAGAGGTTGTTCAATCATGATCACACAAGGAACGGGGCTCGTTTATCACAGTG	1020						
Db	961	CTTTTGAGAGGTTGTTTCAATCATGATCACACAAGGAACGGGGCTCGTTTATCACAGTG	1020						
QY	1021	AGGAGCAGACGTGAGCCCCCGCTGCACCTCTGCTGTAAACACCCAGCATCCCTT	1080						

Db	1021	AGGAGCAGACGTGAGCCCCCGCTGCACCTCTGCTGTAAACACCCAGCATCCCTT	1080						
QY	1081	CTTTCAAAAAGGATCTTTTATAGAGAAACACACTGAGAGATATCTGAAGAAATTTGAT	1140						
Db	1081	CTTTCAAAAAGGATCTTTTATAGAGAAACACACTGAGAGATATCTGAAGAAATTTGAT	1140						
QY	1141	TCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGTAA	1200						
Db	1141	TCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAATTAAGTAA	1200						
QY	1201	AAGCTAGTCTTAACCTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTAAATTAAGT	1260						
Db	1201	AAGCTAGTCTTAACCTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTAAATTAAGT	1260						
QY	1261	GTAAGTAAACATTAACATTTGTATGATGGAACATGGAAGAACATTAACAGTGTCT	1320						
Db	1261	GTAAGTAAACATTAACATTTGTATGATGGAACATGGAAGAACATTAACAGTGTCT	1320						
QY	1321	ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA	1380						
Db	1321	ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA	1380						
QY	1381	AAATGCTTATCATTAAGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATG	1440						
Db	1381	AAATGCTTATCATTAAGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATG	1440						
QY	1441	TAGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTAT	1500						
Db	1441	TAGTTATTTCTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTAT	1500						
QY	1501	ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT	1560						
Db	1501	ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT	1560						
QY	1561	TATTTACACTCTTGAATTTCTCAAAATGAGAAATGAGAAATGAGAAATTTGATGTTGA	1620						
Db	1561	TATTTACACTCTTGAATTTCTCAAAATGAGAAATGAGAAATGAGAAATTTGATGTTGA	1620						
QY	1621	TAAAGTCAAGTGAACAGAGTGAATTTGTTGCATCCAGGCCCTTTTGTCTTGGTGTATG	1680						
Db	1621	TAAAGTCAAGTGAACAGAGTGAATTTGTTGCATCCAGGCCCTTTTGTCTTGGTGTATG	1680						
QY	1681	ATCTCCCTTAAGCATTCCAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA	1740						
Db	1681	ATCTCCCTTAAGCATTCCAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA	1740						
QY	1741	GAAAAGTTTCACTGTATTTGAATCAGATGCCCTTCACTGAAAAAACAATATCCAAATA	1800						
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QY	1801	ATGAGAAATGTGTGGCTCACATCGTAGAGTCCAGAGGGACAGTCAAGTTTAAAGGTTGC	1860						
Db	1801	ATGAGAAATGTGTGGCTCACATCGTAGAGTCCAGAGGGACAGTCAAGTTTAAAGGTTGC	1860						
QY	1861	CTGTATCCAGTAACCTCGGGGCTGTTCCTCCCGTGGGCTCTGTGGCTGTACAGCTTTCCTT	1920						
Db	1861	CTGTATCCAGTAACCTCGGGGCTGTTCCTCCCGTGGGCTCTGTGGCTGTACAGCTTTCCTT	1920						
QY	1921	CTCCATGTGTGATTCTCTCAGGCTGGTAGCAAGTTCTGATCTTATACCCACACACA	1980						
Db	1921	CTCCATGTGTGATTCTCTCAGGCTGGTAGCAAGTTCTGATCTTATACCCACACACA	1980						
QY	1981	CAGCAACATCCAGAAATAAAGTTCT	2005						
Db	1981	CAGCAACATCCAGAAATAAAGATCT	2005						

RESULT 3
US-09-967-305-4
; Sequence 4, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:

; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIORITY FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(1235)
US-09-967-305-4

Query Match 99.9%; Score 2003.4; DB 10; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGTGGGCTTAAGGGCTGCTCAGTTTCCTTCAGCGGGGACATGGGAA 60
Db 25 TTGCAGGCTGTGGGCTTAAGGGCTGCTCAGTTTCCTTCAGCGGGGACATGGGAA 84
QY 61 GCGCCATGGCACTGAGGCGATCTCGGTGAGAGCTGTCGGCCCTGGCCCGGCGGT 120
Db 85 GCGCCATGGCACTGAGGCGATCTCGGTGAGAGCTGTCGGCCCTGGCCCGGCGGT 144
QY 121 TCTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 145 TCTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
QY 181 CCCGCTACGACGTGAGCCGCTTGGGCGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGC 240
Db 205 CCCGCTACGACGTGAGCCGCTTGGGCGGCGGCAAGCGCTCGCTAGTGTGACCTGAAGC 264
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Db 265 AGCCGGGGGAGCGCCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGC 324
QY 301 CCTTCCCGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 325 CCTTCCCGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
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Db 385 ATCCAAGGCTTATTATGCAAGGCTGAGTGATTTGCCAGTCAAGGAAGCTTCTGCGCGT 444
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Db 445 TAGCTGGCCACGATATCAACTATTGGCTTTGTGCAAGTGTCTCTCAAAAATGGCAGAA 504
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Db 865 TGAGCATGATGATGGCCAGAAATGAGAAGAGTTTGACAGATGATTTGCAAGAAGA 924
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Db 1105 CTTTCAAAAGGATCCTTTCATAGGAGAACACACACTGAGAGATACCTGGAAGATTGGAT 1164
QY 1141 TCAGCCCGGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGGTAA 1200
Db 1165 TCAGCCCGGAAGAGATTATCAGCTTAACCTCAGATAAATCATTTGAAAGTAAAGGTAA 1224
QY 1201 AAGCTAGTCTCTAAGTCCAGGCCCCACGGCTCAAGTGAATTTGAATACCTGCAATTACAGT 1260
Db 1225 AAGCTAGTCTCTAAGTCCAGGCCCCACGGCTCAAGTGAATTTGAATACCTGCAATTACAGT 1284
QY 1261 GTAGAGTAACACATTAACATTTGATGATGGAACATGGAAGAACAGTATTACAGTGTCT 1320
Db 1285 GTAGAGTAACACATTAACATTTGATGATGGAACATGGAAGAACAGTATTACAGTGTCT 1344
QY 1321 ACCACTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTATGATGATGATTTCTAA 1380
Db 1345 ACCACTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTATGATGATGATTTCTAA 1404
QY 1381 AATGCTTATCATTAAGGCTTTGATTTATAAACCTTGGGTACTTATACTAAATTTATGG 1440
Db 1405 AATGCTTATCATTAAGGCTTTGATTTATAAACCTTGGGTACTTATACTAAATTTATGG 1464
QY 1441 TAGTTATCTGCTTCCAGTTTGCTGATATATTTGATATTTAAGATTCTGACTTAT 1500
Db 1465 TAGTTATCTGCTTCCAGTTTGCTGATATATTTGATATTTAAGATTCTGACTTAT 1524
QY 1501 ATTTGAATGGTTCATGTAAGAAAGAAATGATATATTCTTGAAGACATGATATACATT 1560
Db 1525 ATTTGAATGGTTCATGTAAGAAAGAAATGATATATTCTTGAAGACATGATATACATT 1584
QY 1561 TATTTACACTCTTGATTTCAATGTAGAAATGAGAAATGCCACAATTTGATGGTGA 1620
Db 1585 TATTTACACTCTTGATTTCAATGTAGAAATGAGAAATGCCACAATTTGATGGTGA 1644
QY 1621 TAAAGTCAAGTGAAGACAGTATTTGTTGCATCCAGGCCCTTTGTCTTGGTGTTCATG 1680
Db 1645 TAAAGTCAAGTGAAGACAGTATTTGTTGCATCCAGGCCCTTTGTCTTGGTGTTCATG 1704
QY 1681 ATCTCCCTTAAGCACATTCCAAACCTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1740
Db 1705 ATCTCCCTTAAGCACATTCCAAACCTTTAGCAACAGTTATCACACTTTGTAATTTGCAAA 1764
QY 1741 GAAAGTTTCACTGTATGAAATCAGAAATGCGCTTCACTGAAAAAACAATATCCAAATA 1800
Db 1765 GAAAGTTTCACTGTATGAAATCAGAAATGCGCTTCACTGAAAAAACAATATCCAAATA 1824
QY 1801 ATGAGGAATGTGTGGCTCACTACGTAGAGTCCAGAGGACAGTCAAGTTTAAAGGTTGC 1860

Db 1825 ATGAGGAAATGTTGGCTCACTACGTAGAGTCCAGAGGACAGTCACTTTTAGGGTTGC 1884
QY 1861 CTGTATCCAGTAACCTGGGGCCCTGTTTCCCGTGGGTCTCTGGGCTGTCAAGCTTTCTTT 1920
Db 1885 CTGTATCCAGTAACCTGGGGCCCTGTTTCCCGTGGGTCTCTGGGCTGTCAAGCTTTCTTT 1944
QY 1921 CTCATGTGTTGATTTCTCCACAGGCTGGTAGCAAGTCTGTGATCTTATACCAACACA 1980
Db 1945 CTCATGTGTTGATTTCTCCACAGGCTGGTAGCAAGTCTGTGATCTTATACCAACACA 2004
QY 1981 CAGCAACATCCAGAAATAAGTCT 2005
Db 2005 CAGCAACATCCAGAAATAAGATCT 2029

RESULT 4
US-09-967-305-8
: Sequence 8, Application US/09967305
: Patent No. US20020123081A1
: GENERAL INFORMATION:
: APPLICANT: Richardson, Jennifer
: APPLICANT: Monahan, John
: TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
: FILE REFERENCE: 07334-312001
: CURRENT APPLICATION NUMBER: US/09/967,305
: PRIOR APPLICATION NUMBER: 2001-09-28
: PRIOR FILING DATE: 2000-09-28
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 3023
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (90)...(683)
US-09-967-305-8

Query Match 83.4%; Score 1671.4; DB 10; Length 3023;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1843; Conservative 0; Mismatches 1; Indels 161; Gaps 1;
QY 1 TTGCAGGCTGCTGGGCTGGGGCTAAGGCTGCTCAAGTTCTCTCAGCGGGGCACTGGGAA 60
Db 25 TTGCAGGCTGCTGGGCTGGGGCTAAGGCTGCTCAAGTTCTCTCAGCGGGGCACTGGGAA 84
QY 61 GCGCCATGGCACTGACAGGCACTCTCGTGTGAGCTGTCCGGCTGGCCCGGCGCGT 120
Db 85 GCGCCATGGCACTGACAGGCACTCTCGTGTGAGCTGTCCGGCTGGCCCGGCGCGT 144
QY 121 TCTGTGCTATGCTCTGGCTGACCTTCGGGGCGCGTGTGTACCGGTGACCGCGCGCGT 180
Db 145 TCTGTGCTATGCTCTGGCTGACCTTCGGGGCGCGTGTGTACCGGTGACCGCGCGCGT 204
QY 181 CCGGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGACCTGAAGC 240
Db 205 CCGGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTGTGCTGACCTGAAGC 264
QY 241 AGCCGCGGGGAGCCCGCTGCTGCGCGCGTGTGTGCAAGCGGTGCGATGTGCTGTGAGC 300
Db 265 AGCCGCGGGGAGCCCGCTGCTGCGCGCGTGTGTGCAAGCGGTGCGATGTGCTGTGAGC 324
QY 301 CCTCCGCGCGGTGTCTATGAGAAACTCCAGCTGGGGCCAGAGATTTCTGACGGGAAA 360
Db 325 CCTCCGCGCGGTGTCTATGAGAAACTCCAGCTGGGGCCAGAGATTTCTGACGGGAAA 384
QY 361 ATCCAAAGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAAAGCTTCTGCCGT 420
Db 385 ATCCAAAGCTTATTTATGCCAGGCTGAGTGAATTTGGCCAGTCAAGAAAGCTTCTGCCGT 444
QY 421 TAGCTGGCCACGATATCAACTATTGGCTTTGTGACGGTGTCTCTCAAAAATTGGCAGAA 480

Db 445 TAGCTGGCCACGATATCAACTATTGGCTTTGTCA----- 479
QY 481 GTGTGAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGCTGTGGGCTTAA 540
Db 480 ----- 479
QY 541 TGTGTGACGTGGGATTTAATGCTCTTTTGAACCGACACGCACTGGCAAGGTCAGG 600
Db 480 ----- 479
QY 601 TCATTGATGCAATATGTTGGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAATC 660
Db 480 -----GGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGAAAATC 523
QY 661 AGAAATCGAGTCTGTGGGAAGCACCTCGAGACAGAAACATGTTGATGTTGAGCACCTT 720
Db 524 AGAAATCGAGTCTGTGGGAAGCACCTCGAGACAGAAACATGTTGATGTTGAGCACCTT 583
QY 721 TCTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAACAATAGAACCC 780
Db 584 TCTATACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAACAATAGAACCC 643
QY 781 AGTTCTACGAGCTGCTGATCAAGACCTTGACATAAGTCTGATGAACCTCCCAATCAGA 840
Db 644 AGTTCTACGAGCTGCTGATCAAGACCTTGACATAAGTCTGATGAACCTCCCAATCAGA 703
QY 841 TGACATGATGATTTGGCCAGAAATGAAGAAGAACTTTGCAGATGATTTTGCAGAAAGA 900
Db 704 TGACATGATGATTTGGCCAGAAATGAAGAAGAACTTTGCAGATGATTTTGCAGAAAGA 763
QY 901 CGAAGCAGAGTGTGTCAATCTTTGACGCGACAGATGCCCTGTGTGACTCCGGTCTGA 960
Db 764 CGAAGCAGAGTGTGTCAATCTTTGACGCGACAGATGCCCTGTGTGACTCCGGTCTGA 823
QY 961 CTTTGAAGAGTGTCTCATCATGATCACAACAAGAAAGGGGCTGTTTATCACCAGTG 1020
Db 824 CTTTGAAGAGTGTCTCATCATGATCACAACAAGAAAGGGGCTGTTTATCACCAGTG 883
QY 1021 AGGACGAGAGCTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 1080
Db 884 AGGACGAGAGCTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 943
QY 1081 CTTCAAAAAGGATCCTTTCATAGAGAAACACACTGAGAGATTTGAAGATTTGGAT 1140
Db 944 CTTCAAAAAGGATCCTTTCATAGAGAAACACACTGAGAGATTTGAAGATTTGGAT 1003
QY 1141 TCAGCCCGGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTAAGTAAGGTAA 1200
Db 1004 TCAGCCCGGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTAAGTAAGGTAA 1063
QY 1201 AAGCTAGTCTTAATTTCCAGGCGCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGT 1260
Db 1064 AAGCTAGTCTTAATTTCCAGGCGCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGT 1123
QY 1261 GTAGAGTAACACATTAATTTGATGATGGAACATGAGGAACATTAACAGTGTCTCT 1320
Db 1124 GTAGAGTAACACATTAATTTGATGATGGAACATGAGGAACATTAACAGTGTCTCT 1183
QY 1321 ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAA 1380
Db 1184 ACCACTTAATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAA 1243
QY 1381 AAATGGTTATCATTAAGGCTTTGATTTTAAACTTTGGGTACTTAAATTAATG 1440
Db 1244 AAATGGTTATCATTAAGGCTTTGATTTTAAACTTTGGGTACTTAAATTAATG 1303
QY 1441 TAGTTATTCGCTTCAGAGTTTGGTTGATATATTTGATATTAAGATTTCTGACTTAT 1500
Db 1304 TAGTTATTCGCTTCAGAGTTTGGTTGATATATTTGATATTAAGATTTCTGACTTAT 1363
QY 1501 ATTTGAATGGTCTAGTGAAGAAGAAATGATATATTTCTGAAGACATGATATACAT 1560

Db 1364 ATTTGAATGGGTCTAGTGA AAAAGGAATGATATATTCTTGAAGACATCGATATACATT 1423

QY 1561 TATTTACACTCTTGATTCTTACAAATGTAGAAAATGAGGAATGCCACAATTTGATGTGA 1620

Db 1424 TATTTACACTCTTGATTCTTACAAATGTAGAAAATGAGGAATGCCACAATTTGATGTGA 1483

QY 1621 TAAAGTCACGTGAAAACAGAGTGTGTTGCATCCAGGCCCTTTTGTCTTGGTTCATG 1680

Db 1484 TAAAGTCACGTGAAAACAGAGTGTGTTGCATCCAGGCCCTTTTGTCTTGGTTCATG 1543

QY 1681 ATCTCCCTCTAAGCACATTCCAAACCTTTAGCAACAGTTATACACTTTGTAAATTGCAAA 1740

Db 1544 ATCTCCCTCTAAGCACATTCCAAACCTTTAGCAACAGTTATACACTTTGTAAATTGCAAA 1603

QY 1741 GAAAAGTTTCACCTGTATGAAATCAGAATGCCCTTCAACTGAAAAAACAATATCCAAAATA 1800

Db 1604 GAAAAGTTTCACCTGTATGAAATCAGAATGCCCTTCAACTGAAAAAACAATATCCAAAATA 1663

QY 1801 ATGAGGAAATGTGTGGCTCAGTACGTAGAGTCCAGAGGGACAGTCAGTTTAGGTTGC 1860

Db 1664 ATGAGGAAATGTGTGGCTCAGTACGTAGAGTCCAGAGGGACAGTCAGTTTAGGTTGC 1723

QY 1861 CTGTATCCAGTAACTCGGGGCCCTGTTCCTCCCGTGGGTCTCTGGGCTGTACGCTTCCCTT 1920

Db 1724 CTGTATCCAGTAACTCGGGGCCCTGTTCCTCCCGTGGGTCTCTGGGCTGTACGCTTCCCTT 1783

QY 1921 CTCAATGTGTGATTCTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCCAACACA 1980

Db 1784 CTCAATGTGTGATTCTCTCTCAGGCTGTAGCAAGTTCTGATCTTATACCCAACACA 1843

QY 1981 CAGCAACATCCAGAAATAAGTTCT 2005

Db 1844 CAGCAACATCCAGAAATAAGATCT 1868

RESULT 5

US-09-232-880-107

; Sequence 107, Application US/09232880

; Publication No. US20020182596a1

; GENERAL INFORMATION:

; APPLICANT: Xu, JIANGCHUN

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.428C6

; CURRENT APPLICATION NUMBER: US/09/232, 880

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-232-880-107

Query Match 78.5%; Score 1574.2; DB 9; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGTCTGAGAGTGTCCGGCCTGGCCCCGGCCCGCTT 121

Db 1 CGCCATGGCACTGCAGGGCATCTCGTCTGAGAGTGTCCGGCCTGGCCCCGGCCCGCTT 60

QY 122 CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTTACGCGTGGACCGCGGCTC 181

Db 61 CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTTACGCGTGGACCGCGGCTC 120

QY 182 CCGCTACGAGCTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCA 241

Db 121 CCGCTACGAGCTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTCTGAGCTGAAGCA 180

QY 242 GCCGCGGGGAGCCCGCTGCTGCGCGCTCTGTGCAAGCGGTGGATGTGCTGTGAGCC 301

Db 181 GCCGCGGGGAGCCCGCTGCTGCGCGCTCTGTGCAAGCGGTGGATGTGCTGTGAGCC 240

QY 302 CTTCGCGCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGA AAA 361

Db 241 CTTCGCGCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGA AAA 300

QY 362 TCCAGGCTTATTATGCCAGGCTGAGTGAGTTGGCCAGTCAGGAAGCTTCTGCCGCTT 421

Db 301 TCCAGGCTTATTATGCCAGGCTGAGTGAGTTGGCCAGTCAGGAAGCTTCTGCCGCTT 360

QY 422 AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAG 481

Db 361 AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAG 420

QY 482 TGGTGAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGGTGGCTTAT 541

Db 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGGTGGCTTAT 480

QY 542 GTGTGCACTGGGCATTATATAGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGT 601

Db 481 GTGTGCACTGGGCATTATATAGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGT 540

QY 602 CATGTATGCAAAATATGTTGGAAGAACAGCATATTTAAGTTCTTTCTGTGAAAACTCA 661

Db 541 CATGTATGCAAAATATGTTGGAAGAACAGCATATTTAAGTTCTTTCTGTGAAAACTCA 600

QY 662 GAAATCGAGTCTGTGGAGCACTCGAGGACAGAAACATGTGGATGTGAGCACCTTT 721

Db 601 GAAATCGAGTCTGTGGAGCACTCGAGGACAGAAACATGTGGATGTGAGCACCTTT 660

QY 722 CTATACGACTTACAGGACAGACAGATGGGGAATTCATGGCTTTGGAGCAATAGAACCCCA 781

Db 661 CTATACGACTTACAGGACAGACAGATGGGGAATTCATGGCTTTGGAGCAATAGAACCCCA 720

QY 782 GTTCTACGAGCTGCTGATCAAAAGCACTTGACTTAAAGTCTGATGAACCTCCCAATCAGAT 841

Db 721 GTTCTACGAGCTGCTGATCAAAAGCACTTGACTTAAAGTCTGATGAACCTCCCAATCAGAT 780

QY 842 GAGCATGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTGCCAAAGAGAGAC 901

Db 781 GAGCATGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTGCCAAAGAGAGAC 840

QY 902 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC 961

Db 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC 900

QY 962 TTTTGAAGAGTGTGTTCATCATGATCAACAAGGAAGCGGCTGTTTATCACCAGTGA 1021

Db 901 TTTTGAAGAGTGTGTTCATCATGATCAACAAGGAAGCGGCTGTTTATCACCAGTGA 960

QY 1022 GGAGCAGAGCTGAGCCCCCGCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTC 1081

Db 961 GGAGCAGAGCTGAGCCCCCGCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTC 1020

QY 1082 TTTCAAAAAGGATCTTTCATAGAGAACACACTGAGGAGATCTTGAAGAATTTGATTT 1141

Db 1021 TTTCAAAAAGGATCTTTCATAGAGAACACACTGAGGAGATCTTGAAGAATTTGATTT 1080

QY 1142 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCAATTTGAAGTAAATAGGTAAA 1201

Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCAATTTGAAGTAAATAGGTAAA 1140

QY 1202 AGCTAGTCTCTAACTTCCAGGCCACAGGCTCAAGTGAATTTGAATTAATTAACATG 1261

Db 1141 AGCTAGTCTCTAACTTCCAGGCCACAGGCTCAAGTGAATTTGAATTAATTAACATG 1200

QY 1262 TAGAGTAACACATTAACATTTGTATGCATGGAACATGAGAGAACAGTATTACAGTGTCTTA 1321

Db 1201 TAGAGTAACACATTAACATTTGTATGCATGGAACATGAGAGAACAGTATTACAGTGTCTTA 1260

QY 1322 CCACTCTAATCAAGAAAAAGAAATTAAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1381

Db 1322 CCACTCTAATCAAGAAAAAGAAATTAAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1381

Db 1261 CCACTCTAATCAAGAAAAGAAATACAGACTCTGATTTCTACAGATGATGATGAATTCCTAAA 1320
 QY 1382 AATGGTATCATTAGGGCTTTTGATTTATATAAACTTTGGGACTTATACTAAATTTATGGT 1441
 Db 1321 AATGGTATCATTAGGGCTTTTGATTTATATAAACTTTGGGACTTATACTAAATTTATGGT 1380
 QY 1442 AGTTATTCCTGCTTCCAGTTTTCCTGATATATTTGTGATATTTAAGATTTCTGACTTATA 1501
 Db 1381 AGTTATTCCTGCTTCCAGTTTTCCTGATATATTTGTGATATTTAAGATTTCTGACTTATA 1440
 QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1561
 Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
 QY 1562 ATTTACACTCTTGATTTCTACATGTAGAAAATGAGGAAATGCCACAATTTGTATGCTGAT 1621
 Db 1501 ATTTACACTCTTGATTTCTACATGTAGAAAATGAGGAAATGCCACAATTTGTATGCTGAT 1560
 QY 1622 AAAAGTCACGTGAACAGAGA 1640
 Db 1561 AAAAGTCACGTGAACAGAGA 1579

RESULT 6

US-10-012-896-107
 : Sequence 107, Application US/10012896
 : Publication No. US20020183251A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yujin
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Darick
 : APPLICANT: Li, Samuel X.
 : APPLICANT: Wang, Aljun
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Hepler, William T.
 : APPLICANT: Henderson, Robert A.
 : APPLICANT: Hural, John
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Houghton, Raymond L.
 : APPLICANT: Vinals de Bassols, Carlota
 : APPLICANT: Foy, Teresa
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Wantanabe, Yoshihiro
 : APPLICANT: Meagher, Madeleine Joy
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : FILE REFERENCE: 210121.427C27
 : CURRENT APPLICATION NUMBER: US/10/012,896
 : NUMBER OF SEQ ID NOS: 1011
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 107
 : LENGTH: 1621
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-10-012-896-107

Query Match 78.5%; Score 1574.2; DB 9; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGCGACAGGAGGATCTCGGTCTGTGAGCTGTCCGGCTTGCCCGGCGCCGCTT 121
 Db 1 CGCCATGCGACAGGAGGATCTCGGTCTGTGAGCTGTCCGGCTTGCCCGGCGCCGCTT 60

QY 122 CTGTCTATGCTCTCGGCTGACTTCGGGGCGGCTGTGTGACCGCTGAGCCGGCCCGCTC 181
 Db 61 CTGTCTATGCTCTCGGCTGACTTCGGGGCGGCTGTGTGACCGCTGAGCCGGCCCGCTC 120
 QY 182 CCGCTACGAGCTGAGCCCGCTTGGGGCGGGCGCAAGCGCTGCTAGTGTGACCTGAAGCA 241
 Db 121 CCGCTACGAGCTGAGCCCGCTTGGGGCGGGCGCAAGCGCTGCTAGTGTGACCTGAAGCA 180
 QY 242 GCCGGGGGAGCCCGGCTGCTGGCGGCTGTGCAAGCGGTGGATGTGCTGTGAGCC 301
 Db 181 GCCGGGGGAGCCCGGCTGCTGGCGGCTGTGCAAGCGGTGGATGTGCTGTGAGCC 240
 QY 302 CTTCGCGCGCGGTGTCAATGAGAACTCCAGCTGGGGCCAGAGATTCGACGCGGAGAA 361
 Db 241 CTTCGCGCGCGGTGTCAATGAGAACTCCAGCTGGGGCCAGAGATTCGACGCGGAGAA 300
 QY 362 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTT 421
 Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGTT 360
 QY 422 AGCTGGCCAGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAA 481
 Db 361 AGCTGGCCAGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAA 420
 QY 482 TGGTGAATCCGTATGCCCGCGCTGAATCTCTGCTGACTTTGCTGTGCTGCTTAT 541
 Db 421 TGGTGAATCCGTATGCCCGCGCTGAATCTCTGCTGACTTTGCTGTGCTGCTTAT 480
 QY 542 GTGTGACCTGGCATTTATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGT 601
 Db 481 GTGTGACCTGGCATTTATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGT 540
 QY 602 CATGATGCAAAATATGTTGGAAGGAACACATATTTAACTTTTCTGTGAAAACCTCA 661
 Db 541 CATGATGCAAAATATGTTGGAAGGAACACATATTTAACTTTTCTGTGAAAACCTCA 600
 QY 662 GAAATGAGTCTGTGGAGACACCTCGAGACAGAACATGTTGATGTTGGAAGCACCCTT 721
 Db 601 GAAATGAGTCTGTGGAGACACCTCGAGACAGAACATGTTGATGTTGGAAGCACCCTT 660
 QY 722 CTATACGACTTACAGACACAGATGGGGAATTCATGCTGTGTGAGCAATAGAACCCCA 781
 Db 661 CTATACGACTTACAGACACAGATGGGGAATTCATGCTGTGTGAGCAATAGAACCCCA 720
 QY 782 GTTCTACGAGCTGTGATCAAAAGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 841
 Db 721 GTTCTACGAGCTGTGATCAAAAGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 780
 QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAGAAAGTTTGCAGATGATTTGCCAAAAGAGAC 901
 Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAGAAAGTTTGCAGATGATTTGCCAAAAGAGAC 840
 QY 902 GAAGCAGAGTGTGTCAAACTTTTGACGCGCACAGATGCTGTGTGACTCCGGTCTGAC 961
 Db 841 GAAGCAGAGTGTGTCAAACTTTTGACGCGCACAGATGCTGTGTGACTCCGGTCTGAC 900
 QY 962 TTTTGAAGAGTGTTCATCATGATGATCACAACAAGAGAGGGGCTGTTTATCACCAGTGA 1021
 Db 901 TTTTGAAGAGTGTTCATCATGATGATCACAACAAGAGAGGGGCTGTTTATCACCAGTGA 960
 QY 1022 GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTPAAAACCCCAAGCCATCCCTTC 1081
 Db 961 GGAGCAGAGCTGAGCCCGCCCTGACCTCTGCTGTTPAAAACCCCAAGCCATCCCTTC 1020
 QY 1082 TTTCAAAAGGATCTTTCTATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGATTT 1141
 Db 1021 TTTCAAAAGGATCTTTCTATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGATTT 1080
 QY 1142 CAGCCGGAAGAGATTTATCAGCTTAACCTAGATTAATAATTAATTAAGGTAA 1201
 Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACCTAGATTAATAATTAATTAAGGTAA 1140
 QY 1202 AGCTAGTCTTAACCTTCAGAGCCCAAGGCTCAAGTGAATTTGAATTAAGTCAATTTACAGTG 1261

|||||
Db 1141 AGCTAGTCTTAACCTCCAGGCCACGCGCTCAAGTGAATTGAACTACTGCATTACAGTG 1200
QY 1262 TAGAGTAACACATACATTTGTATGCATGGAACATGAGAACAGTATTACAGTGTCTTA 1321
|||||
Db 1201 TAGAGTAACACATACATTTGTATGCATGGAACATGAGAACAGTATTACAGTGTCTTA 1260
QY 1322 CCACTCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTGATGATGAAATCTTAA 1381
|||||
Db 1261 CCACTCTAATCAAGAAAGATTTACAGACTCTGATTTCTACAGTGATGATGAAATCTTAA 1320
QY 1382 AATGTTATCATTAGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGCT 1441
|||||
Db 1321 AATGTTATCATTAGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGCT 1380
QY 1442 AGTTATCTGCTTCCAGTTTGGCTGATATATTTGTTGATATTAGATTTCTGACTTATA 1501
|||||
Db 1381 AGTTATCTGCTTCCAGTTTGGCTGATATATTTGTTGATATTAGATTTCTGACTTATA 1440
QY 1502 TTTGGAATGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1561
|||||
Db 1441 TTTGGAATGGTTCTAGTGAAGAAAGGAATGATATTTCTTGAAGACATCGATATACATTT 1500
QY 1562 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAATGCCACAAATTTGATGCTGAT 1621
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Db 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAATGCCACAAATTTGATGCTGAT 1560
QY 1622 AAAAGTCACGTGAACAGA 1640
|||||
Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 7
US-09-895-793-107
; Sequence 107, Application US/09895793
; Publication No. US20020192763A1.
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-107

Query Match 78.5%; Score 1574.2; DB 9; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CGCCATGGACATGACGGCATCTCGCTGAGACTGTCCGGCTGGCCCGCCGGCTT 121
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Db 1 CGCCATGGACATGACGGCATCTCGCTGAGACTGTCCGGCTGGCCCGCCGGCTT 60
QY 122 CTGTGCTATGCTGCTGCTGACTTTCGGGGCGGCTGTGTACGCGTGAGCCGGCCGGCTC 181
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Db 61 CTGTGCTATGCTGCTGCTGACTTTCGGGGCGGCTGTGTACGCGTGAGCCGGCCGGCTC 120
QY 182 CCGCTACGACGTGAGCCGCTTGGCGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCA 241
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Db 121 CCGCTACGACGTGAGCCGCTTGGCGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCA 180
QY 242 GCCCGGGGAGCCCGCTGCTGCGGCGCTGTGTGCAAGCGGTCGATGTCTGTGAGCC 301
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Db 181 GCCCGGGGAGCCCGCTGCTGCGGCGCTGTGTGCAAGCGGTCGATGTCTGTGAGCC 240
QY 302 CTTCGGCGCGGCTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGACCGGGAAGA 361
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Db 241 CTTCGGCGCGGCTGTATGAGAGAACTCCAGCTGGGCCAGAGATTCTGACCGGGAAGA 300
QY 362 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTT 421
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Db 301 TCCAAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTT 360
QY 422 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTCTCTCAAAAAATGGCAGAAG 481
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Db 361 AGCTGGCCACGATATCACTATTTGGCTTTGTGAGGTCTCTCTCAAAAAATGGCAGAAG 420
QY 482 TGGTGAGAAATCCGATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTTAT 541
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Db 421 TGGTGAGAAATCCGATGCCCGCTGATCTCTGCTGCTGCTGCTGCTGCTTAT 480
QY 542 GTGTGCACTGGCATTTAATGCGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGT 601
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Db 481 GTGTGCACTGGCATTTAATGCGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGT 540
QY 602 CATGTATCAAAATATGCTGGAAGAACAGACATATTTAAGTCTTTTGTGAAAACTCA 661
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Db 541 CATGTATCAAAATATGCTGGAAGAACAGACATATTTAAGTCTTTTGTGAAAACTCA 600
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Db 601 GAAATCGAGTCTGTGGAAGCACCTCGAGGACAAACATGTTGATGGTGAGCACTTT 660
QY 722 CTATACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGAGCAATAGAACCCCA 781
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Db 661 CTATACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 841
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Db 721 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 780
QY 842 GAGCATGATGATGGCCGAATGAAGAAGAGCTTTCAGATGTATTTCGAAGAAGAGAC 901
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Db 781 GAGCATGATGATGGCCGAATGAAGAAGAGCTTTCAGATGTATTTCGAAGAAGAGAC 840
QY 902 GAAGCAGAGTGGTCAAAATCTTTGACGGGACAGATGCTGTGTGACTCCGGTCTGAC 961
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Db 841 GAAGCAGAGTGGTCAAAATCTTTGACGGGACAGATGCTGTGTGACTCCGGTCTGAC 900
QY 962 TTTTGAAGAGTTTTCATCATGATCACAACAAGAAAGGGGCTGCTTATACCAAGTGA 1021
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Db 901 TTTTGAAGAGTTTTCATCATGATCACAACAAGAAAGGGGCTGCTTATACCAAGTGA 960
QY 1022 GGAGCAGAGCGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTC 1081
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Db 961 GGAGCAGAGCGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGATT 1141
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Db 1021 TTTCAAAAGGCGATCCTTTCATAGAGAACACACTGAGAGATACTTGAGAATTTGGATT 1080
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Db 1081 CAGCCGCGAAGAGATTATTCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAGGTAAA 1140
QY 1202 AGCTAGTCTTAACCTTCAGGCCACGCGCTCAAGTGAATTTGAATACATTTACAGTG 1261
Db 1141 AGCTAGTCTTAACCTTCAGGCCACGCGCTCAAGTGAATTTGAATACATTTACAGTG 1200
QY 1262 TAGAGTAACACATTAACATTTGATGATGGAACATGAGGAACAGTATTACAGTGTCTA 1321
Db 1201 TAGAGTAACACATTAACATTTGATGATGGAACATGAGGAACAGTATTACAGTGTCTA 1260
QY 1322 CCACTCTAATCAAGAAAAAGATTACAGACTCTGATTTACAGTGATGATGAATTTCTAAA 1381
Db 1261 CCACTCTAATCAAGAAAAAGATTACAGACTCTGATTTACAGTGATGATGAATTTCTAAA 1320
QY 1382 AATGTTATCATTAGGGCTTTGATTTATAAACTTTGGGTACTTATTAATTAATGAT 1441
Db 1321 AATGTTATCATTAGGGCTTTGATTTATAAACTTTGGGTACTTATTAATTAATGAT 1380
QY 1442 AGTTATTCCTGCTTCCAGCTTTGCTGATATTTGTTGATATTAAGATTTCTGACTTATA 1501
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Db 1501 ATTTACACTCTGATTTACATGTAGAAAAAGAGAAATGCCAACAAATTTGATGATGAT 1560
QY 1622 AAAAGTCACGTGAACACA 1640
Db 1561 AAAAGTCACGTGAACACA 1579

RESULT 8
US-09-895-814-107
; Sequence 107, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepner, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-107
Query Match 78.5%; Score 1574.2; DB 9; length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CGCCATGGCAGCTGACGGCATCTCGGTGCTGAGCTGTCCGGCCCGCCCGCCGCTT 121
Db 1 CGCCATGGCAGCTGACGGCATCTCGGTGCTGAGCTGTCCGGCCCGCCCGCCGCTT 60
QY 122 CTGTGCTATGCTCCTGCTGACTTGGGGGGCGCGGTGTGTGTACGCGGTGAGACCGCGCGCTC 181
Db 61 CTGTGCTATGCTCCTGCTGACTTGGGGGGCGCGGTGTGTGTACGCGGTGAGACCGCGCGCTC 120
QY 182 CCGCTACGACGTGAGCCGCTTGGCGCGGGGCAAGCCGCTCGTACGTGTGACCTGAAGCA 241
Db 121 CCGCTACGACGTGAGCCGCTTGGCGCGGGGCAAGCCGCTCGTACGTGTGACCTGAAGCA 180
QY 242 GCCCGGGGAGCCCGCTGCTGCGCGCTCTGTGCAACCGGTGATGTGCTGTGAGCC 301
Db 181 GCCCGGGGAGCCCGCTGCTGCGCGCTCTGTGCAACCGGTGATGTGCTGTGAGCC 240
QY 302 CTTCGCGCGCGGTGTATGAGAACTCCAGCTGGCGCCAGAGATTCTGCAGCGGAGAAA 361
Db 241 CTTCGCGCGCGGTGTATGAGAACTCCAGCTGGCGCCAGAGATTCTGCAGCGGAGAAA 300
QY 362 TCCAGGCTTATTTATGCCAGGCTGATGATTTGGCCAGTCAAGAACTTCTGCCGCTT 421
Db 301 TCCAGGCTTATTTATGCCAGGCTGATGATTTGGCCAGTCAAGAACTTCTGCCGCTT 360
QY 422 AGCTGGCCAGATATCAACTATTTGGCTTGTGACAGGTGTTCTCTCAAAAATTGGCAGAG 481
Db 361 AGCTGGCCAGATATCAACTATTTGGCTTGTGACAGGTGTTCTCTCAAAAATTGGCAGAG 420
QY 482 TGGTGAATCCGATATGCCCGCGCTGATCTCTGCTGACTTTGCTGCTGCTGCTTAT 541
Db 421 TGGTGAATCCGATATGCCCGCGCTGATCTCTGCTGACTTTGCTGCTGCTGCTTAT 480
QY 542 GTGTGACTGGGCATTTAATGCTTTTGTGACCGCACGCACTGGCCAAAGGTCAGGT 601
Db 481 GTGTGACTGGGCATTTAATGCTTTTGTGACCGCACGCACTGGCCAAAGGTCAGGT 540
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Db 541 CATGTATGCAATATGCTGGAAGACAGCATATTTAAGTCTTTCTGTGGAAGACTCA 600
QY 662 GAAATCGAGTCTGTGGAAGCACCTGAGGACAGACATGTTGATGCTGAGACCTTT 721
Db 601 GAAATCGAGTCTGTGGAAGCACCTGAGGACAGACATGTTGATGCTGAGACCTTT 660
QY 722 CTATACGACTTACAGACAGCAGATGGGGAATTTCATGGCTGTTGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGACAGCAGATGGGGAATTTCATGGCTGTTGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGACTTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCTGATGACTTCCCAATCAGAT 780
QY 842 GAGCATGATGATGGCCAGAAATGAAGAAGATTGACATGTTTGGCAAGAGAGAC 901
Db 781 GAGCATGATGATGGCCAGAAATGAAGAAGATTGACATGTTTGGCAAGAGAGAC 840
QY 902 GAAGGAGAGTGTGCTCAATCTTGAACGGGACAGATGCTGTGTGACTCCGGTTCTGAC 961
Db 841 GAAGGAGAGTGTGCTCAATCTTGAACGGGACAGATGCTGTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGAGAGGTGTTTCATCATGATCAACAAGAAAGGGGCTGCTTATCAGCAGTGA 1021
Db 901 TTTTGAGAGGTGTTTCATCATGATCAACAAGAAAGGGGCTGCTTATCAGCAGTGA 960

OY	1022	GGAGCAGGACGTGAGCCCCCGCCCTGCACCCTCTGCTGTAAACACCCCGAGCCATTCCTTC 	1081
Db	961	GGAGCAGGACGTGAGCCCCCGCCCTGCACCCTCTGCTGTAAACACCCCGAGCCATTCCTTC 	1020
OY	1082	TTTCAAAAAGGATCCTTTCATAGGAGAACAACACTGAGAGATACTTGAAGAATTTCGATT 	1141
Db	1021	TTTCAAAAAGGATCCTTTCATAGGAGAACAACACTGAGAGATACTTGAAGAATTTCGATT 	1080
OY	1142	CAGCCGCCAAGAGATTTATCAGCTTAACCTCAGATTAATCATTTGAAGTAATAGCTAAA 	1201
Db	1081	CAGCCGCCAAGAGATTTATCAGCTTAACCTCAGATTAATCATTTGAAGTAATAGCTAAA 	1140
OY	1202	AGCTAGTCTCTAACCTCCAGGCCCGCCGCTCAAGTGAAATTTGAATACTGCATTTACAGTG 	1261
Db	1141	AGCTAGTCTCTAACCTCCAGGCCCGCCGCTCAAGTGAAATTTGAATACTGCATTTACAGTG 	1200
OY	1262	TAGAGTAACACATPAACATTTGTATGCATGGAACAATGAGCAACAGTATTACAGTGTCTTA 	1321
Db	1201	TAGAGTAACACATPAACATTTGTATGCATGGAACAATGAGCAACAGTATTACAGTGTCTTA 	1260
OY	1322	CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTGAATTTCTAAA 	1381
Db	1261	CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGATGATTGAATTTCTAAA 	1320
OY	1382	AATGGTTATCATTAGGGCTTTTGATTATATAAACCTTGGGTACTTATACTAAATTATGGT 	1441
Db	1321	AATGGTTATCATTAGGGCTTTTGATTATATAAACCTTGGGTACTTATACTAAATTATGGT 	1380
OY	1442	AGTTATTCTGCCCTTCCAGTTTGCTTGATATATTTGTTGATATTTAAGATTCTTGACTTATA 	1501
Db	1381	AGTTATTCTGCCCTTCCAGTTTGCTTGATATATTTGTTGATATTTAAGATTCTTGACTTATA 	1440
OY	1502	TTTTGAATGGTCTCTAGTGA AAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 	1561
Db	1441	TTTTGAATGGTCTCTAGTGA AAAAAGGAATGATATATTTCTTGAAGACATCGATATACATTT 	1500
OY	1562	ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAAATTTGTATGGTGAT 	1621
Db	1501	ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAAATTTGTATGGTGAT 	1560
OY	1622	AAAAGTCACGTGAACAGAA 1640 	
Db	1561	AAAAGTCACGTGAACAGAA 1579 	

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RESULT 9
US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759, 143
; CURRENT FILING DATE: 2001-01-12

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; NUMBER OF SEQ ID NOS: 934 '
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
;
US-09-759-143-107

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Query Match	78.5%;	Score 1574.2;	DB 10;	Length 1621;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1576; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	62	CGCCATGGCACTGCAGGCGCATCTCGGTCTGTGGAGCTGTCCGGCTGGCCCCCGGGCCCGTT	121
Db	1	CGCCATGGCACTGCAGGCGCATCTCGGTCTATGGAGCTGTCCGGCTGGCCCCCGGGCCCGTT	60
QY	122	CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTACCGGTGGACCGGCCGCGTC	181
Db	61	CTGTGCTATGCTCTGGCTGACTTCGGGGCGCGTGTGTACCGGTGGACCGGCCGCGTC	120
QY	182	CCGCTACGACGTGAGCCGCTTGGGCCCGGGGCAAGCCGTCGCTAGTCTGGACCTGAAGCA	241
Db	121	CCGCTACGACGTGAGCCGCTTGGGCCCGGGGCAAGCCGTCGCTAGTCTGGACCTGAAGCA	180
QY	242	GCCGCGGGAGCCCGCGTCTGCGCGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCC	301
Db	181	GCCGCGGGAGCCCGCGTCTGCGCGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCC	240
QY	302	CTTCCGCGCGGCTGTCAATGAGAAACTCCAGCTGGGCCACAGATTTCTGACGGGAAAA	361
Db	241	CTTCCGCGCGGCTGTCAATGAGAAACTCCAGCTGGGCCACAGATTTCTGACGGGAAAA	300
QY	362	TCCAAGGCTATTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	421
Db	301	TCCAAGGCTATTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360
QY	422	AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAG	481
Db	361	AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAG	420
QY	482	TGCTGAGAATCCGTATGCCCGCTGAATCTCTCGGCTGACTTTGCTGTGTGGCCTTAT	541
Db	421	TGCTGAGAATCCGTATGCCCGCTGAATCTCTCGGCTGACTTTGCTGTGTGGCCTTAT	480
QY	542	GCTGTCACTGGGCATTATTAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGT	601
Db	481	GCTGTCACTGGGCATTATTAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGT	540
QY	602	CATTGATGCAAAATATGTGTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA	661
Db	541	CATTGATGCAAAATATGTGTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA	600
QY	662	GAATCGAGTCTGTGGAGACACCTCGAGGACAGAACATGTTGGATGTTGGAGCACCTTT	721
Db	601	GAATCGAGTCTGTGGAGACACCTCGAGGACAGAACATGTTGGATGTTGGAGCACCTTT	660
QY	722	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	781
Db	661	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720
QY	782	GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT	841
Db	721	GTTCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT	780
QY	842	GAGCATGATGATTGGCCAGAAATGAAGAAGATTGACATGTATTTGCAAAAGAAGAC	901
Db	781	GAGCATGATGATTGGCCAGAAATGAAGAAGATTGACATGTATTTGCAAAAGAAGAC	840
QY	902	GAAGGACAGTGTGTCAAACTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC	961
Db	841	GAAGGACAGTGTGTCAAACTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC	900
QY	962	TTTTGAGGAGTTGTTCATCATGATCACAAACAAGGAACGGGCTCGTTATCACCAGTGA	1021

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Db 901 TTTGAGAGGTTGTTTCATCATGATCACAACAAGGAGCGGCTCGTTTATCACACAGTGA 960
QY 1022 GGAGCAGAGCTGAGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1081
Db 961 GGAGCAGAGCTGAGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
QY 1082 TTTCAAAAGGATCCCTTTCATAGAGAGACACACATGAGAGATTAAGATTTGGATT 1141
Db 1021 TTTCAAAAGGATCCCTTTCATAGAGAGACACACATGAGAGATTAAGATTTGGATT 1080
QY 1142 CAGCCGCGAAGAGATTATACAGCTTAAGTAAATCATTTGAAGTAAAGTAAAGTAA 1201
Db 1081 CAGCCGCGAAGAGATTATACAGCTTAAGTAAATCATTTGAAGTAAAGTAAAGTAA 1140
QY 1202 AGCTAGTCTTAACCTTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTAAAGTAA 1261
Db 1141 AGCTAGTCTTAACCTTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTAAAGTAA 1200
QY 1262 TAGAGTAACACATTAACATTTGATGATGAAGACATGAGAGACAGTATTAAGTAAAGTAA 1321
Db 1201 TAGAGTAACACATTAACATTTGATGATGAAGACATGAGAGACAGTATTAAGTAAAGTAA 1260
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Db 1261 CCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTATGATGATGATGAT 1320
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QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTTGAAGACATCGATATACATTT 1561
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QY 1562 ATTTACACTCTGATTTCTACAAATGTAGAAAATGAGAAATGCCAATTTGATGATGAT 1621
Db 1501 ATTTACACTCTGATTTCTACAAATGTAGAAAATGAGAAATGCCAATTTGATGATGAT 1560
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Db 1561 AAAAGTCACGTCGAACAAA 1579

RESULT 10
US-09-780-669-107
; Sequence 107, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-107

Query Match 78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGTGTGAGAGCTGTCCGGCCCTGGCCCGGGCCGCTT 121
Db 1 CGCCATGGCACTGCAGGGCATCTCGTGTGAGAGCTGTCCGGCCCTGGCCCGGGCCGCTT 60
QY 122 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
Db 61 CTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 182 CCGCTACGAGCTGAGCCGCTTGGGCGCGGCGCAAGCGCTGCTAGTGTGCTGCACTGAAGCA 241
Db 121 CCGCTACGAGCTGAGCCGCTTGGGCGCGGCGCAAGCGCTGCTAGTGTGCTGCACTGAAGCA 180
QY 242 GCCGCGGGAGCCGCGCTGCTGCGCGGCTGCTGCAAGCGGTCGATGTGCTGCTGAGCC 301
Db 181 GCCGCGGGAGCCGCGCTGCTGCGCGGCTGCTGCAAGCGGTCGATGTGCTGCTGAGCC 240
QY 302 CTTCGCGCGCGGCTGCTATGAGAAACTCCAGCTGGGCCAGAGATTTGCGAGCGGGA 361
Db 241 CTTCGCGCGCGGCTGCTATGAGAAACTCCAGCTGGGCCAGAGATTTGCGAGCGGGA 300
QY 362 TCCAGGCTATTTATGCCAGCGCTGAGTGTGGCCAGTCAAGAGCTTCTGCCGTT 421
Db 301 TCCAGGCTATTTATGCCAGCGCTGAGTGTGGCCAGTCAAGAGCTTCTGCCGTT 360
QY 422 AGCTGGCAGCATATCAATATTTGGCTTGTCTGAGGTGTCTCTCAAAAAATTTGGCAGA 481
Db 361 AGCTGGCAGCATATCAATATTTGGCTTGTCTGAGGTGTCTCTCTCAAAAAATTTGGCAGA 420
QY 482 TGGTGAATCCGTATGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
Db 421 TGGTGAATCCGTATGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 542 GTGTGCACTGGCATTTATATGCTCTTTTGACCGCACAGCACTGGCAAGGGTCAAGT 601
Db 481 GTGTGCACTGGCATTTATATGCTCTTTTGACCGCACAGCACTGGCAAGGGTCAAGT 540
QY 602 CATTGATGCAATATGCTGGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 661
Db 541 CATTGATGCAATATGCTGGAAGAACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 600
QY 662 GAAATCGAGTCTGTGGGAAGCACTCGAGAGACAGAACATGTTGGATGGTGAGACACCTTT 721
Db 601 GAAATCGAGTCTGTGGGAAGCACTCGAGAGACAGAACATGTTGGATGGTGAGACACCTTT 660
QY 722 CTATACGACTTACAGAGACAGATGGGCAATTCATGGCTTGGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGAGACAGATGGGCAATTCATGGCTTGGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAGAGACTTGAAGTGTGATGAAGTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAGAGACTTGAAGTGTGATGAAGTCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAGAAAGTTTGCAGATGTATTTGCCAAGAAGAC 901
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAGAAAGTTTGCAGATGTATTTGCCAAGAAGAC 840

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QY      902 GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGTGAC    961
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Db      841 GAAAGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGTGAC    900

QY      962 TTTTGAGGAGGTGTTTCATCATGATGCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA    1021
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Db      901 TTTTGAGGAGGTGTTTCATCATGATGCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA    960

QY      1022 GGAGCAGGACGTGAGCCCCCCCCTGCACCTCTGCTTTAAACACCCCGAGCCATCCCTTC    1081
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Db      961 GGAGCAGGACGTGAGCCCCCCCCTGCACCTCTGCTTTAAACACCCCGAGCCATCCCTTC    1020

QY      1082 TTTCAAAAGGAGTCCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGATTGTGATT    1141
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Db      1021 TTTCAAAAGGAGTCCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGATTGTGATT    1080

QY      1142 CAGCCGGGAAGAGATTATTCAGCTTAACCTCAGATTAATCATTTGAAGTAATAAGGTAAA    1201
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Db      1081 CAGCCGGGAAGAGATTATTCAGCTTAACCTCAGATTAATCATTTGAAGTAATAAGGTAAA    1140

QY      1202 AGCTAGTCTCTAAGTTCAGGCCCCCAGGGCTCAAGTGAATTGAACTACTGCATTTACAGTG    1261
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Db      1141 AGCTAGTCTCTAAGTTCAGGCCCCCAGGGCTCAAGTGAATTGAACTACTGCATTTACAGTG    1200

QY      1262 TAGAGTAACACATTAACATTCATGTCATGGAACATGGAGAACAGTATTACAGTGTCCTA    1321
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Db      1201 TAGAGTAACACATTAACATTCATGTCATGGAACATGGAGAACAGTATTACAGTGTCCTA    1260

QY      1322 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTCCTACAGTGATGATTGAATTCCTAAA    1381
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Db      1261 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTCCTACAGTGATGATTGAATTCCTAAA    1320

QY      1382 AATGGTTATCATTAGGGCTTTTGATTATTAACACTTTGGGTACTTATCTAAATTAATGCT    1441
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Db      1321 AATGGTTATCATTAGGGCTTTTGATTATTAACACTTTGGGTACTTATCTAAATTAATGCT    1380

QY      1442 AGTTATTCCTGCCCTCCAGTTTGCTGATATATTTGTTGATATTAAGATTCTTGACTTATA    1501
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Db      1381 AGTTATTCCTGCCCTCCAGTTTGCTGATATATTTGTTGATATTAAGATTCTTGACTTATA    1440

QY      1502 TTTTGAATGGTTCCTAGTGAAAAAGGAATGATATATCTTGAAGACATCGATATACATTT    1561
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QY      1562 ATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGAAATGCCAACAAATTTGATGGTGAT    1621
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Db      1501 ATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGAAATGCCAACAAATTTGATGGTGAT    1560

QY      1622 AAAAGTCACGTGAACACAGA    1640
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Db      1561 AAAAGTCACGTGAACACAAA    1579

RESULT 11
US-09-030-606-107
; Sequence 107, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-606-107

Query Match          78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGGTCTGTGAGAGCTGTCCGGCTGGCCCCGGCCGTT 121
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Db 1 CGCCATGGCACTGCAGGGCATCTCGGTCTGTGAGAGCTGTCCGGCTGGCCCCGGCCGTT 60

QY 122 CTGTGCTATGTGCTCTGCTGCTGACTTCGGGGCGCGGTGTGTACCGCTGGAACGGCCGGCTC 181
    |||||||
Db 61 CTGTGCTATGTGCTCTGCTGCTGACTTCGGGGCGCGGTGTGTGTACCGCTGGAACGGCCGGCTC 120

QY 182 CCGCTACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGTGTGCTGTGACCTGAAGCA 241
    |||||||
Db 121 CCGCTACGACGTGAGCCGCTTGGGGCGGGGCAAGCGCTCGTGTGCTGTGACCTGAAGCA 180

QY 242 GCCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCC 301
    |||||||
Db 181 GCCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCC 240

QY 302 CTTCGGCGCGGGGTGTGTCATGGAGAACTCCAGCTGGGGCCAGAGATTCTGCAGCGGAAA 361
    |||||||
Db 241 CTTCGGCGCGGGGTGTGTCATGGAGAACTCCAGCTGGGGCCAGAGATTCTGCAGCGGAAA 300

QY 362 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTT 421
    |||||||
Db 301 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTT 360

QY 422 AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAA 481
    |||||||
Db 361 AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAAATTGGCAGAA 420

QY 482 TGGTGAAGATCCGATATGCCCGGCTGAATCTCCTGGCTGACCTTGTGCTGTGCGCTTAT 541
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Db 421 TGGTGAAGATCCGATATGCCCGGCTGAATCTCCTGGCTGACCTTGTGCTGTGCGCTTAT 480

QY 542 GTGTGCACCTGGGCATTATATGGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGT 601
    |||||||
Db 481 GTGTGCACCTGGGCATTATATGGCTCTTTTGTGACCGCACACGCACTGACAAAGGTCAGGT 540

QY 602 CATGTATGCAAAATATGTGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGAAAACTCA 661
    |||||||
Db 541 CATGTATGCAAAATATGTGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGAAAACTCA 600

QY 662 GAAATCGAGTCTGTGGAAGCACTCGAGGACAGAACAATGTGATGTGTGAGCACCTTT 721
    |||||||
Db 601 GAAATCGAGTCTGTGGAAGCACTCGAGGACAGAACAATGTGATGTGTGAGCACCTTT 660

QY 722 CTATACGACTTACAGACAGCATGGGGAAATTCATGGCTTTGGAGCAATAGAACCCA 781
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Db 661 CTATACGACTTACAGACAGACAGATGGGAAATTCATGGCTGTTGAGCAATAGAACCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT 780
QY 842 GAGCATGATGATGGCCCAAAATGAAGAAGAGTTTGCAGATGATATTGCAAAAGAAGAC 901
Db 781 GAGCATGATGATGGCCCAAAATGAAGAAGAGTTTGCAGATGATATTGCAAAAGAAGAC 840
QY 902 GAAGCAGAGTGGTGTCAATCTTTGACGGCACAGATGGCTGTGTACCTCCGCTTCTGAC 961
Db 841 GAAGCAGAGTGGTGTCAATCTTTGACGGCACAGATGGCTGTGTACCTCCGCTTCTGAC 900
QY 962 TTTTGAGAGGTTGTTTCATCATGATCACACAAGAACGGGCTCGTTTATCACACAGTGA 1021
Db 901 TTTTGAGAGGTTGTTTCATCATGATCACACAAGAACGGGCTCGTTTATCACACAGTGA 960
QY 1022 GGAGCAGACGTGAGCCCCCCCCCTGCACCTCTGCTGTAAACACCCCAAGCATCCCTTC 1081
Db 961 GGAGCAGACGTGAGCCCCCCCCCTGCACCTCTGCTGTAAACACCCCAAGCATCCCTTC 1020
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Db 1081 CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATTAATAATCATTTGAAGTATTAAGTAAA 1140
QY 1202 AGCTAGTCTTAACCTTCCAGCCCCCAGCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1261
Db 1141 AGCTAGTCTTAACCTTCCAGCCCCCAGCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
QY 1262 TAGAGTACACATTAACATTTGATGCATGGAACCATGGAGAACAGTATTACAGTGTCTTA 1321
Db 1201 TAGAGTACACATTAACATTTGATGCATGGAACCATGGAGAACAGTATTACAGTGTCTTA 1260
QY 1322 CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1381
Db 1261 CCACTCTAATCAAGAAAAAGAAATTACAGACTCTGATTTCTACAGTGAATGAATTTCTAAA 1320
QY 1382 AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTGGTACTTATACTAAATTTATGTT 1441
Db 1321 AATGGTTATCATTTAGGGCTTTTGAATTAATAAACTTTGGTACTTATACTAAATTTATGTT 1380
QY 1442 AGTTATTCGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1501
Db 1381 AGTTATTCGCTTCCAGTTTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440
QY 1502 TTTTGAATGGTCTAGTGAATAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1561
Db 1441 TTTTGAATGGTCTAGTGAATAAAGAAATGATATATTTCTGAAGACATCGATATACATTT 1500
QY 1562 ATTTACACTCTGATTTCTACATGTAGAAAAATGAGAAATGCCACAATTTGATGTGAT 1621
Db 1501 ATTTACACTCTGATTTCTACATGTAGAAAAATGAGAAATGCCACAATTTGATGTGAT 1560
QY 1622 AAAAGTCAGGTGAACAGA 1640
Db 1561 AAAAGTCAGGTGAACAAA 1579

RESULT 12
US-09-822-827-107
; Sequence 107, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-107
Query Match 78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CGCCATGGCACTGCAGGGCATTTCCGTCGTGAGAGCTGTCCGGCCTGGCCCCGGCCGTT 121
Db 1 CGCCATGGCACTGCAGGGCATTTCCGTCGTGAGAGCTGTCCGGCCTGGCCCCGGCCGTT 60
QY 122 CTGTGCTATGCTCCTGGCTGACTTCCGGGCGCTGTGTACCGCTGACCGGCGGCTC 181
Db 61 CTGTGCTATGCTCCTGGCTGACTTCCGGGCGCTGTGTACCGCTGACCGGCGGCTC 120
QY 182 CCGCTACGACGTGAGCCGCTTTGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA 241
Db 121 CCGCTACGACGTGAGCCGCTTTGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180
QY 242 GCCCGGGGAGCCCGCTGCTGCGGCGTGTGTGCAAGCGGTGCGATGTGCTGCTGAGCC 301
Db 181 GCCCGGGGAGCCCGCTGCTGCGGCGTGTGTGCAAGCGGTGCGATGTGCTGCTGAGCC 240
QY 302 CTTCGCGCGGGGTGCATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATA 361
Db 241 CTTCGCGCGGGGTGCATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATA 300
QY 362 TCCAAGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTT 421
Db 301 TCCAAGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTT 360
QY 422 AGCTGGCCAGATATCAACTATTGTGGCTTGTGCAGGTGTCTCTCAAAAAATTGGCAGAAG 481
Db 361 AGCTGGCCAGATATCAACTATTGTGGCTTGTGCAGGTGTCTCTCAAAAAATTGGCAGAAG 420
QY 482 TGGTGAATCCGATATGCCCGCTGAATTCCTGGCTGACTTTGCTGGTGGCCTTAT 541
Db 421 TGGTGAATCCGATATGCCCGCTGAATTCCTGGCTGACTTTGCTGGTGGCCTTAT 480
QY 542 GTGTGCACCTGGGCATTATTAATGGCTCTTTTGACCGCACACGCACTGGCAAGGGTCAGGT 601
Db 481 GTGTGCACCTGGGCATTATTAATGGCTCTTTTGACCGCACACGCACTGGCAAGGGTCAGGT 540
QY 602 CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATAACTCA 661
Db 541 CATTGATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATAACTCA 600
QY 662 GAAATCGAGTCTGTGGAGACACCTCGAGACAGACATGTTGGATGGTGGAGCACCTTT 721
Db 601 GAAATCGAGTCTGTGGAGACACCTCGAGACAGACATGTTGGATGGTGGAGCACCTTT 660
QY 722 CTATACGACTTACAGGACAGATGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGGACAGATGGGAATTCATGGCTGTGTGAGCAATAGAACCCCA 720
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Db 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGAAGTCTGATGAACCTTCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAAATGAAGAAGAGTTTGCAGATGATATTGCAAAAGAAGAC 901
Db 781 GAGCATGATGATTTGGCCAAATGAAGAAGAGTTTGCAGATGATATTGCAAAAGAAGAC 840
QY 902 GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGGCTGTGTGACTCCGGTCTGAC 961
Db 841 GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGGCTGTGTGACTCCGGTCTGAC 900

QY 962 TTTTGAGAGGTTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA 1021
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Db 901 TTTTGAGAGGTTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA 960
QY 1022 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1081
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Db 961 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
QY 1082 TTTCAAAAGGAGTCTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATT 1141
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Db 1021 TTTCAAAAGGAGTCTTTCATAGGAGAACACACTGAGAGATCTTGAAGATTGGATT 1080
QY 1142 CAGCCGCGAAGAGATTATCAGCTTAACCTCAGATAAATCATTGAAAGTAATAGGTAAA 1201
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Db 1081 CAGCCGCGAAGAGATTATCAGCTTAACCTCAGATAAATCATTGAAAGTAATAGGTAAA 1140
QY 1202 AGCTAGTCTCTAAGTCCAGGCCACGCTCAAGTGAATTTGAATACTGCATTACAGTG 1261
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Db 1141 AGCTAGTCTCTAAGTCCAGGCCACGCTCAAGTGAATTTGAATACTGCATTACAGTG 1200
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QY 1322 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGATTTCTAAA 1381
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Db 1261 CCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGATTTCTAAA 1320
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Db 1321 AATGGTATCATTAGGCTTTGATTTATAAACCTTTGGGTACTTATACTAAATATATGCT 1380
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Db 1441 TTTTGAATGGTTCCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
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Db 1501 ATTTACACTCTTGATCTTACAATGTAGAAAAATGAGAAATGCCACAATTTGATGCTGAT 1560
QY 1622 AAAAGTCACGTGAACAGA 1640
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Db 1561 AAAAGTCACGTGAACAGA 1579

RESULT 13
US-09-115-453-107
; Sequence 107, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for windows version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-107

Query Match 78.5%; Score 1574.2; DB 10; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGGTCGTGAGACTGTCCGGCCCTGCCCCGGCCCGTT 121
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Db 1 CGCCATGGCACTGCAGGGCATCTCGGTCATGAGACTGTCCGGCCCTGCCCCGGCCCGTT 60
QY 122 CTGTGCTATGCTCTGCGCTGACTTCGGGGCGCGGTGTGTACGCGTGGACCGCGCGCTC 181
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Db 61 CTGTGCTATGCTCTGCGCTGACTTCGGGGCGCGGTGTGTGTACGCGTGGACCGCGCGCTC 120
QY 182 CCGCTACGACGTGAGCCGCTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
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Db 121 CCGCTACGACGTGAGCCGCTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 242 GCCCGGGGAGCCCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 301
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Db 181 GCCCGGGGAGCCCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCG 240
QY 302 CTTCCGCGCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATTCTGCACCGGGAATA 361
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Db 241 CTTCCGCGCGCGGTGTCATGAGAAACTCCAGCTGGGCCAGAGATTCTGCACCGGGAATA 300
QY 362 TCCAAGGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTCGCGGTT 421
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Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTCGCGGTT 360
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Db 361 AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCTCAAAAATTTGGCAGAA 420
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Db 421 TGGTGAATCCGTATGCCCCCGCTGAATCTCTGCGCTGACTTTGCTGCTGCTGCGCTTAT 480
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Db 481 GTGTGCACTGGGCAATTAATGCTCTTTTGAACCGCACACGCGCTGCGCAAGGGTCAAGT 540
QY 602 CATTGATGCAAAATATGCTGGAAGAACACAGCAATTTAAAGTCTTTCTGTGGAATAAATCTCA 661
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Db 541 CATTGATGCAAAATATGCTGGAAGAACACAGCAATTTAAAGTCTTTCTGTGGAATAAATCTCA 600
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Db 601 GAAATGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGACACCTTT 660
QY 722 CTATACGACTTACAGGACGACGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 781
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Db 661 CTATACGACTTACAGGACGACGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
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Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT 780
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Db 781 GAGCATGATGATGGCCAGAAATGAAGAAGAACTTGCAGATGATTTGCAAAAGAAAGAC 840
QY 902 GAAGCAGAGTGTGTCAAATCTTTGACGGCAGAGATGCTGTGATCCGGTCTGAC 961
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Db 841 GAAGCAGAGTGTGTCAAATCTTTGACGGCAGAGATGCTGTGATCCGGTCTGAC 900
QY 962 TTTTGAAGAGTGTTCATCATGATCACAACAAGAAACGGGGCTCGTTTATCACCAGTGA 1021
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Db 901 TTTTGAAGAGTGTTCATCATGATCACAACAAGAAACGGGGCTCGTTTATCACCAGTGA 960
QY 1022 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTC 1081
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Db 961 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTTTAAACACCCAGCCATCCCTTC 1020
QY 1082 TTTCAAAAGGAGTCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT 1141
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Db 1021 TTTCAAAAGGAGTCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTTGGATT 1080
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Db 1081 CAGCCGCGAAGAGATTTATGAGCTTAAGTAAATCATTTGAAGTAAATAGTAAA 1140
QY 1202 AGCTAGTCTTAAGTCTTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTCTTACAGTG 1261
Db 1141 AGCTAGTCTTAAGTCTTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTCTTACAGTG 1200
QY 1262 TAGAGTAACACATTAACATTTGATGATGGAACATGAGAACAGTATTTACAGTGTCTTA 1321
Db 1201 TAGAGTAACACATTAACATTTGATGATGGAACATGAGAACAGTATTTACAGTGTCTTA 1260
QY 1322 CCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTATGATGAAATTTCTAAA 1381
Db 1261 CCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTATGATGAAATTTCTAAA 1320
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QY 1502 TTTGAATGGGTTCTAGTAAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1561
Db 1441 TTTGAATGGGTTCTAGTAAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1500
QY 1562 ATTTACACTCTTGATTTCTACATGTAGAAAATGAGAAAATGCCAATAATTTGATGTGAT 1621
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QY 1622 AAAAGTCACGTGAACAGA 1640
Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 14
US-09-967-305-6
: Sequence 6, Application US/09967305
: Patent No. US20020123081A1
: GENERAL INFORMATION:
: APPLICANT: Richardson, Jennifer
: APPLICANT: Monahan, John
: TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
: TITLE OF INVENTION: REFRATORY AND METASTATIC PROSTATE CANCERS
: FILE REFERENCE: 07334-312001
: CURRENT FILING DATE: 2001-09-28
: PRIOR APPLICATION NUMBER: US/09/967, 305
: PRIOR FILING DATE: 2000-09-28
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 3654
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (90)...(1271)
US-09-967-305-6

Query Match 59.7%; Score 1197; DB 10; Length 3654;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCAGGCTGCTGGGCTGAGGCTAAGGCTGCTCAGTTTCTTACAGCGGGGCACTGGGAA 60
Db 25 TTGCAGGCTGCTGGGCTGAGGCTAAGGCTGCTCAGTTTCTTACAGCGGGGCACTGGGAA 84
QY 61 GCGGCATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCCTGGCCCCGGCCGCT 120
Db 85 GCGGCATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCCTGGCCCCGGCCGCT 144

QY 121 TCTGTGCTATGCTCTGCTGCTGACTTCTCGGGCGCGTGTGTACCGGTGAGCCGCCGCGCT 180
Db 145 TCTGTGCTATGCTCTGCTGCTGACTTCTCGGGCGCGTGTGTACCGGTGAGCCGCCGCGCT 204
QY 181 CCCGCTACGACGTGAGCCGCTTGGCCGGGGCAAGCCGTCTGCTAGTGTGGAACCTGAAGC 240
Db 205 CCCGCTACGACGTGAGCCGCTTGGCCGGGGCAAGCCGTCTGCTAGTGTGGAACCTGAAGC 264
QY 241 AGCCGCGGGAGCCCGCGCTGCGGCGTCTGTGCAAGCGGTCGGATGTCTGCTGAGC 300
Db 265 AGCCGCGGGAGCCCGCGCTGCGGCGTCTGTGCAAGCGGTCGGATGTCTGCTGAGC 324
QY 301 CCTTCCGCGCGGCTGCTATGAGAAACCTCCAGCTGGGGCCAGAGATTTCTGCAAGCGGAAA 360
Db 325 CCTTCCGCGCGGCTGCTATGAGAAACCTCCAGCTGGGGCCAGAGATTTCTGCAAGCGGAAA 384
QY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTGCCGCT 420
Db 385 ATCCAAGGCTTATTTATGCCAGGCTGAGTGTGATTTGGCCAGTCAGGAAGCTTCTGCCGCT 444
QY 421 TAGCTGGCCAGCATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAA 480
Db 445 TAGCTGGCCAGCATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTGGCAGAA 504
QY 481 GTGTGAGAAATCCGTAATGCCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY 541 TGTGTGCACTGGGCTATTAATGCGCTTTTGTGACCCGACACGCACTGGCAAGGCTCAGG 600
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QY 601 TCATTGATCAAAATATGTTGGAAGAAAGCAACATATTTAACTCTTTCTGTGTGAAAATCTC 660
Db 625 TCATTGATCAAAATATGTTGGAAGAAAGCAACATATTTAACTCTTTCTGTGTGAAAATCTC 684
QY 661 AGAATCGAGCTCTGTGGGAAGCACTCTCGAGACAGAACATGTTGGATGTTGAGCACCTT 720
Db 685 AGAATCGAGCTCTGTGGGAAGCACTCTCGAGACAGAACATGTTGGATGTTGAGCACCTT 744
QY 721 TCTATACGACTTACAGACAGACAGATGGGAAATTCATGCTGTTGAGCAATAGAACCCC 780
Db 745 TCTATACGACTTACAGACAGACAGATGGGAAATTCATGCTGTTGAGCAATAGAACCCC 804
QY 781 AGTTCTACAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 840
Db 805 AGTTCTACAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 864
QY 841 TGAGCATGATGATTTGGCCAGAAATGAAGAGAAGTTTGAGATGATTTGCAAGAAGA 900
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QY 901 CGAAGGCAAGTGTGTCAAAATCTTTGAGCGCACAGATGCTGTGTGACTCCGTTCTGA 960
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QY 961 CTTTGTGAGAGCTTGTTCATCATGATCAACAACAAGAACGGGCTCGTTATTCACAGTG 1020
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QY 1021 AGGACAGAGCTGAGCCCGCCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTT 1080
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QY 1081 CTTTCAAAAAGGATCTTTTCAATAGGAGAACACACTGAGGAGATTAATTGAAGATTGGAT 1140
Db 1105 CTTTCAAAAAGGATCTTTTCAATAGGAGAACACACTGAGGAGATTAATTGAAGATTGGAT 1164
QY 1141 TCAGCCGCGAAGAGATTTATCAGCTTAACCTAGATTAATAATCATTTGAAGATTAATAGG 1197
Db 1165 TCAGCCGCGAAGAGATTTATCAGCTTAACCTAGATTAATAATCATTTGAAGATTAATAGG 1221

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RESULT 15
US-09-967-305-3
; Sequence 3, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLAACYL-CoA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1146)
US-09-967-305-3
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Query Match 57.2%; Score 1146; DB 10; Length 1146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 66 ATGGCACTGCAGGCACTCGGTGCGTGAGAGTGTCCGGCCTGGCCCCGGCGTTCGTGT 125
Db 1 ATGGCACTGCAGGCACTCGGTGCGTGAGAGTGTCCGGCCTGGCCCCGGCGTTCGTGT 60

QY 126 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACCGGTGACCGCGCCGGCTCCGC 185
Db 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACCGGTGACCGCGCCGGCTCCGC 120

QY 186 TACGACGTGAGCCGCTGGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG 245
Db 121 TACGACGTGAGCCGCTGGGGCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG 180

QY 246 CGGGGAGCCGCGTGTGTCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 305
Db 181 CGGGGAGCCGCGTGTGTCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240

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QY 606 GATGCAATATATGTTGAAGAACAGCATATTAACTTTCTTCTGTGAAAACCTCAGAAA 665
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QY 666 TCGAGTCTGTGGAGACACTCGAGGACAGAACATGTTGGATGGTGAGCACCTTTCTAT 725
Db 601 TCGAGTCTGTGGAGACACTCGAGGACAGAACATGTTGGATGGTGAGCACCTTTCTAT 660
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QY 726 ACGACTTACAGACAGACAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 785
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QY 786 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCATGTAAGTCTCCCAATCAGATGAGC 845
Db 721 TACGAGCTGCTGATCAAGAGACTTGGACTAAAGTCATGTAAGTCTCCCAATCAGATGAGC 780

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Db 781 ATGATGATTTGGCCAGAAATGAAGAGAGATTGCGATGTATTGGCAAGAGACGGAAG 840

QY 906 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT 965
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QY 966 GAGGAGTGTGTCATCATGATCAACAACAAGGAACGGGCTGTTATCACCAGTGAAGAG 1025
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QY 1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTCTTC 1085
Db 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTCTTC 1020

QY 1086 AAAAGGATCCTTTTCATAGAGAGACACACACTGAGAGATACTTGAAGATTTGATTCAGC 1145
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QY 1206 AGTCTC 1211
Db 1141 AGTCTC 1146
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Search completed: April 2, 2003, 02:29:58
Job time : 193.983 secs

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 QY 182 CCGCTACGACGTGAGCCGCTTGGGGCGGCGCAAGCGCTCGCTAGTCTGTGACCTGAACA 241
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 QY 242 GCCGGGGGAGCCCGCTGCTGCGGCTGTGTGCAAGCGCTCGGATGTGCTGTGAGCC 301
 Db 181 GCCGGGGGAGCCCGCTGCTGCGGCTGTGTGCAAGCGCTCGGATGTGCTGTGAGCC 240
 QY 302 CTTCGGCGCGGTGTCAAGCAAACTCCAGCTGGCGCCAGAGATTCTGACGGGAAAA 361
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 Db 421 TGGTGAAATCCGTATGCCCCGCTGAATCTCTGCTGACTTTGCTGTGTGCTGCTTAT 480
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 QY 662 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTGGATGGTGAGCACTTT 721
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 QY 722 CTATACGACTTACAGCAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCCA 781
 Db 661 CTATACGACTTACAGCAGCAGATGGGGAATTCATGCTGTGGAGCAATAGAACCCCA 720
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 Db 721 GTTCTACGAGCTGTGATCAAAAGGACTTGACTTAAAGTCTGTGATGAACCTTCCAAATCAGAT 780
 QY 842 GAGCATGATGATGGCCAGAAATGAAGAAGATTGCAAGATGATTTGCAAGAAGAC 901
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 QY 902 GAAGCAGAGTGTGTCAAAATCTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGAC 961
 Db 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGAC 900
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QY 1202 AGTAGTCTCTAAGTCCAGGCCCCACGGCTCAAGTGAATTTGAATACGATTTACAGTG 1261
 Db 1141 AGTAGTCTCTAAGTCCAGGCCCCACGGCTCAAGTGAATTTGAATACGATTTACAGTG 1200
 QY 1262 TAGAGTAACACATTAATGATGATGATGGAACATGAGGAACAGTATTACAGTGTCTA 1321
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 QY 1502 TTTTGAATGGTCTAGTGAAGAAAGGAATGATATATTTCTGAAGACATCGATATACATT 1561
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 QY 1562 ATTTACACTCTGATTTCAATGTAGAAATGAGAAATGCCACAAATTTGATGTGAT 1621
 Db 1501 ATTTACACTCTGATTTCAATGTAGAAATGAGAAATGCCACAAATTTGATGTGAT 1560
 QY 1622 AAAAGTCACGTGAACAGA 1640
 Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 2
 US-09-030-607-107
 ; Sequence 107, Application US/09030607
 ; Patent No. 6262245
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
 ; NUMBER OF SEQUENCES: 224
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/030,607
 ; FILING DATE: 25-FEB-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.427C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 107:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1621 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; ORIGINAL SOURCE:

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; ORGANISM: Homo sapiens
US-09-030-607-107

Query Match          78.5%; Score 1574.2; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGACAGGCGATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGCTT 121
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Db 1 CGCCATGGCACTGACAGGCGATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGCTT 60

QY 122 CTGTGCTATGGTCCCTGGCTGACTTCGGGGCGCGCTGTGTGTAACCGGTGACCCGGCGCTC 181
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Db 61 CTGTGCTATGGTCCCTGGCTGACTTCGGGGCGCGCTGTGTGTAACCGGTGACCCGGCGCTC 120

QY 182 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAGCA 241
    |||||||
Db 121 CCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAGCA 180

QY 242 GCCGGGGGAGCCCGCGTCTGCGGGCTCTGTGCAAGCGGTGCGATGTCTGTGAGCC 301
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Db 181 GCCGGGGGAGCCCGCGTCTGCGGGCTCTGTGCAAGCGGTGCGATGTCTGTGAGCC 240

QY 302 CTTCGGCGCGGTGTGATGGAGAAATCCAGCTGGGCCAGAGATTCGTGACGGGGA 361
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    |||||||
Db 301 TCCAAGGCTTATTTATGCCCAGGCTGAGTGTGATTTGCCAGTCAAGAACTTCTGCCG 360

QY 422 AGCTGGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAAATTTGGCAGA 481
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QY 482 TGGTGAATCCGTATGCCCCGCTGAATCTCCTGCTGACTTTGCTGTGGTGGCTTAT 541
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QY 782 GTTCTACGAGCTGTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGAT 841
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QY 842 GAGCATGATGATGGCCAGAAATGAGAAGAAGTTCAGATGTATTTGCCAAGAAGAC 901
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Db 781 GAGCATGATGATGGCCAGAAATGAGAAGAAGTTCAGATGTATTTGCCAAGAAGAC 840

QY 902 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGAC 961
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Db 841 GAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGAC 900

QY 962 TTTTGAGAGAGTGTGTATCATGATCAACAAGAAGAGGGGCTCGTTTATCACCAGTGA 1021
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Db 901 TTTTGAGAGAGTGTGTATCATGATCAACAAGAAGAGGGGCTCGTTTATCACCAGTGA 960

QY 1022 GGAGCAGACGTGAGCCCGCGCTGCACTCTGCTGTTAAACACCCAGCATCCCTTC 1081
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Db 961 GGAGCAGACGTGAGCCCGCGCGCTGCACCTCTGCTGTTAAACACCCAGCATCCCTTC 1020

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QY 1142 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAGCTAAA 1201
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Db 1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAGCTAAA 1140

QY 1202 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATTAAGTAACTGACGTG 1261
    |||||||
Db 1141 AGCTAGTCTCTAATCTCCAGGCCACGGCTCAAGTGAATTTGAATTAAGTAACTGACGTG 1200

QY 1262 TAGAGTAACACATTAACATTTGTATGCATGGAACATGGAAGAACGTATTACAGTGTCTTA 1321
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Db 1201 TAGAGTAACACATTAACATTTGTATGCATGGAACATGGAAGAACGTATTACAGTGTCTTA 1260

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Db 1261 CCACCTCTAATCAAGAAAGAATTTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAA 1320

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Db 1321 AATGTTATCATTTAGGCGCTTTTGAATTTATAAAACTTTGGTACTTATTAATAATATAGT 1380

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Db 1381 AGTTATTTCTGCCCTCCAGTTTGCCTTGATATATTTGTGATATTAAGATTCTTGACTTATA 1440

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QY 1622 AAAAGTCACGTGAACAGA 1640
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Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 3
US-09-605-785-107
; Sequence 107, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
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; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-107

Query Match 78.5%; Score 1574.2; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 62 CGCCATGGCACTGCAGGGCATCTCGTCTGAGCTGTCCGGCTGGCCCCGGCCCGTT 121
Db 1 CGCCATGGCACTGCAGGGCATCTCGTCTGAGCTGTCCGGCTGGCCCCGGCCCGTT 60
QY 122 CTGTGCTATGCTCTGCTGACTTCGGGGCCGCTGTGTGTAAGCGGTGAGCCGGCCGCTC 181
Db 61 CTGTGCTATGCTCTGCTGACTTCGGGGCCGCTGTGTGTAAGCGGTGAGCCGGCCGCTC 120
QY 182 CCGCTACGACGTGAGCCGCTTGGCCGGGGCAAGCGCTCGTAGTGTGAGCTGAAGCA 241
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QY 242 GCCGGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGATGTGCTGTGAGCC 301
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Db 241 CTTCCGGCCGGGTGTGATGAGAACTCCAGCTGGGCCCAAGATTTCTGACGGGAAAA 300
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Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAAAGCTTGCCTGTT 360
QY 422 AGCTGGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTTGGCAGAAG 481
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Db 421 TGGTGAGATCCGTATGCCCGCTGATCTCTGCTGCTGACTTTGCTGCTGCTGCTTAT 480
QY 542 GTGTGCACTGGGCTTATTAATGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGGT 601
Db 481 GTGTGCACTGGGCTTATTAATGCTCTTTTGAACCGCACACGCACTGGCAAGGCTCAGGT 540
QY 602 CATTGATGCAAAATATGTTGGAAGGAACAGCAATTTAAAGTTCTTTCTGTGAAAACTCA 661
Db 541 CATTGATGCAAAATATGTTGGAAGGAACAGCAATTTAAAGTTCTTTCTGTGAAAACTCA 600
QY 662 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 721
Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTT 660
QY 722 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGTGATCAAAAGGACTTGAATAAGTCTGATGAACCTTCCAATCAGAT 841
Db 721 GTTCTACGAGCTGTGATCAAAAGGACTTGAATAAGTCTGATGAACCTTCCAATCAGAT 780
QY 842 GAGCATGATGATGGCCAGAAATGAAGAAAGAGTTTGACAGATGATTTGCAAAAGAGAC 901
Db 781 GAGCATGATGATGGCCAGAAATGAAGAAAGAGTTTGACAGATGATTTGCAAAAGAGAC 840
QY 902 GAAGGACAGTGTGTCAAAATCTTTGACGGGACAGATGCCGTGTGACTCCGGTTCTGAC 961
Db 841 GAAGGACAGTGTGTCAAAATCTTTGACGGGACAGATGCCGTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGAGGAGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTATCACCACTGA 1021
Db 901 TTTTGAGGAGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTATCACCACTGA 960

QY 1022 GGAGCAGACGTGAGCCCCCCCCCTGCACCTCTGTGTAAACACCCAGCCATFCCCTTC 1081
Db 961 GGAGCAGACGTGAGCCCCCCCCCTGCACCTCTGTGTAAACACCCAGCCATFCCCTTC 1020
QY 1082 TTTCAAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1141
Db 1021 TTTCAAAAGGATCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATT 1080
QY 1142 CAGCCGGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAGGTAAA 1201
Db 1081 CAGCCGGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAGGTAAA 1140
QY 1202 AGCTAGTCTTAACCTTCCAGGCCACGGCTCAAGTGAATTTGAATACCTGATTTACAGTG 1261
Db 1141 AGCTAGTCTTAACCTTCCAGGCCACGGCTCAAGTGAATTTGAATACCTGATTTACAGTG 1200
QY 1262 TAGAGTAACACATTAATGATGATGGAACATGGAAGCAAGATTAACAGTGTCTTA 1321
Db 1201 TAGAGTAACACATTAATGATGATGGAACATGGAAGCAAGATTAACAGTGTCTTA 1260
QY 1322 CCACTCTAATCAAGAAAGAATTACAGACTGTGATTTCTACAGTATGATGATTAATCTTAAA 1381
Db 1261 CCACTCTAATCAAGAAAGAATTACAGACTGTGATTTCTACAGTATGATGATTAATCTTAAA 1320
QY 1382 AATGGTATCATTAAGGCTTTTGATTTATAAACTTTGGGTACTTATACTAAATATATGTT 1441
Db 1321 AATGGTATCATTAAGGCTTTTGATTTATAAACTTTGGGTACTTATACTAAATATATGTT 1380
QY 1442 AGTTATTCGCTTCCAGTTTGTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1501
Db 1381 AGTTATTCGCTTCCAGTTTGTCTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440
QY 1502 TTTGAATGGGTCTAGTGAAGAAAGGAATGATATTTCTGAAGACATGATATACATTT 1561
Db 1441 TTTGAATGGGTCTAGTGAAGAAAGGAATGATATTTCTGAAGACATGATATACATTT 1500
QY 1562 ATTTACACTCTTGTATCTACAATGTAGAAAATGAGAAATGCCACAAATTTGATGTTGAT 1621
Db 1501 ATTTACACTCTTGTATCTACAATGTAGAAAATGAGAAATGCCACAAATTTGATGTTGAT 1560
QY 1622 AAAAGTCACGTGAACAGA 1640
Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 4
US-09-439-313-107
; Sequence 107, Application us/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107

Query Match		78.5%;	Score 1574.2;	DB 4;	Length 1621;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1576;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	62	CGCCATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGGTT	121		
Db	1	CGCCATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGGTT	60		
OY	122	CTGTGCTATGGTCCCTGGCTGACTTCGGGGCGCGTGTGTGACGCGTGAACCGGGCCGCTC	181		
Db	61	CTGTGCTATGGTCCCTGGCTGACTTCGGGGCGCGTGTGTGACGCGTGAACCGGGCCGCTC	120		
OY	182	CCGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	241		
Db	121	CCGCTACGACGTGAGCGGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCA	180		
OY	242	GCCGGGGGAGCGCCCGCTGCTGGCGGCTGTGTCAAGCGGTCGGATGTGCTGTGAGCC	301		
Db	181	GCCGGGGGAGCGCCCGCTGCTGGCGGCTGTGTCAAGCGGTCGGATGTGCTGTGAGCC	240		
OY	302	CTTCCGGCGGCTGTCAATGAGAGAAATCCAGCTGGGGCCAGAGATTCTGCAGCGGAGAA	361		
Db	241	CTTCCGGCGGCTGTCAATGAGAGAAATCCAGCTGGGGCCAGAGATTCTGCAGCGGAGAA	300		
OY	362	TCCAAGGCTTATTTATGCCAGAGGCTGATGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	421		
Db	301	TCCAAGGCTTATTTATGCCAGAGGCTGATGATTTGGCCAGTCAGGAAGCTTCTGCCGTT	360		
OY	422	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAG	481		
Db	361	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAATTTGGCAGAG	420		
OY	482	TGGTAGAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTTGTGTGTGTGCTGTAT	541		
Db	421	TGGTAGAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTTGTGTGTGTGCTGTAT	480		
OY	542	GTGTGCACTGGGCAATTAATAGGCTTTTGTGACCCGACACGCACTGGCAAGGTCAGT	601		
Db	481	GTGTGCACTGGGCAATTAATAGGCTTTTGTGACCCGACACGCACTGGCAAGGTCAGT	540		
OY	602	CATTGATGCAAAATATGTGGAAGGAACGATATTTAACTTTCTTTGTGAAAACTCA	661		
Db	541	CATTGATGCAAAATATGTGGAAGGAACGATATTTAACTTTCTTTGTGAAAACTCA	600		
OY	662	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGACACCTTT	721		
Db	601	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACTGTTGGATGGTGGACACCTTT	660		
OY	722	CTATACGACTTACAGAGACGATGGGGAATTCATGGCTGTTGAGCAATAGAACCCCA	781		
Db	661	CTATACGACTTACAGAGACGATGGGGAATTCATGGCTGTTGAGCAATAGAACCCCA	720		
OY	782	GTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT	841		
Db	721	GTTCTACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTTCCCAATCAGAT	780		
OY	842	GAGCATGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAGAAGAC	901		
Db	781	GAGCATGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAGAAGAC	840		
OY	902	GAAGGACAGTGGTGTCAAAATCTTTGAGGGCACAGATGCTGTGACTCCGGTTCGAC	961		
Db	841	GAAGGACAGTGGTGTCAAAATCTTTGAGGGCACAGATGCTGTGACTCCGGTTCGAC	900		
OY	962	TTTGTAGAGGTTGTTCATCATGATCAACAAGGAAGGGGCTCGTTTATCACCAGTGA	1021		
Db	901	TTTGTAGAGGTTGTTCATCATGATCAACAAGGAAGGGGCTCGTTTATCACCAGTGA	960		
OY	1022	GGAGCAGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCGACCATCCCTTC	1081		
Db	961	GGAGCAGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCGACCATCCCTTC	1020		

OY	1082	TTTCAAAAGGATCTTTCATAGAGAAACACACTGAGAGATACTTGAAATTTGGATT	1141		
Db	1021	TTTCAAAAGGATCTTTCATAGAGAAACACACTGAGAGATACTTGAAATTTGGATT	1080		
OY	1142	CAGCCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAA	1201		
Db	1081	CAGCCCGGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAA	1140		
OY	1202	AGTAGTCTCTAACTTCCAGGCCAGCGGCTCAAGTGAATTTGAATTAAGTACAGTG	1261		
Db	1141	AGTAGTCTCTAACTTCCAGGCCAGCGGCTCAAGTGAATTTGAATTAAGTACAGTG	1200		
OY	1262	TAGAGTAACACATTAATGATGATGGAACATGGAAGAGATTTACAGTGTCTTA	1321		
Db	1201	TAGAGTAACACATTAATGATGATGGAACATGGAAGAGATTTACAGTGTCTTA	1260		
OY	1322	CCACTCTAATCAAGAAAGATTAACAGACTCTGATTTCTACAGTATGATTTCTAAA	1381		
Db	1261	CCACTCTAATCAAGAAAGATTAACAGACTCTGATTTCTACAGTATGATTTCTAAA	1320		
OY	1382	AATGTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATGTT	1441		
Db	1321	AATGTTATCATTTAGGGCTTTTGAATTTATAAACTTTGGTACTTATTAATTAATGTT	1380		
OY	1442	AGTTATTTCTGCCCTTCCAGTTTGGCTGATATATTTGTGATTAAGATTTCTGACTATA	1501		
Db	1381	AGTTATTTCTGCCCTTCCAGTTTGGCTGATATATTTGTGATTAAGATTTCTGACTATA	1440		
OY	1502	TTTTGAATGGTTCAGTGAAGAAAGAAATGATATTTCTTGAAGACATGATATACATTT	1561		
Db	1441	TTTTGAATGGTTCAGTGAAGAAAGAAATGATATTTCTTGAAGACATGATATACATTT	1500		
OY	1562	ATTTACACTCTTGTATTTCAATGTAGAAATGAGAAATGCCACAATTTGTATGTGAT	1621		
Db	1501	ATTTACACTCTTGTATTTCAATGTAGAAATGAGAAATGCCACAATTTGTATGTGAT	1560		
OY	1622	AAAAGTCACGTGAACAGA 1640			
Db	1561	AAAAGTCACGTGAACAAA 1579			

RESULT 5

US-09-352-616A-107

; Sequence 107, Application US/09352616A

; Patent No. 6395278

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jang, Yuguil

; APPLICANT: Xu, Jlangchun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.427C8

; CURRENT APPLICATION NUMBER: US/09/352, 616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-352-616A-107

Query Match		78.5%;	Score 1574.2;	DB 4;	Length 1621;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1576;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	62	CGCCATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGGTT	121		
Db	1	CGCCATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCCGGCGCCCGGCGGTT	60		
OY	122	CTGTGCTATGGTCCCTGGCTGACTTCGGGGCGCGTGTGTGACGCGTGAACCGGGCCGCTC	181		

|||||
 Db 61 CTGTCTATGTTCTGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTC 120
 QY 182 CCGCTACGACGTGAGCCGCTGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 241
 Db 121 CCGCTACGACGTGAGCCGCTGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCA 180
 QY 242 GCCGGGGGAGCCGCGTGTGCGCGCTGTGTGCAAGCGGTGCGATGTGTGAGCC 301
 Db 181 GCCGGGGGAGCCGCGTGTGCGCGCTGTGTGCAAGCGGTGCGATGTGTGAGCC 240
 QY 302 CTTCGGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAA 361
 Db 241 CTTCGGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAA 300
 QY 362 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGGTT 421
 Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGGTT 360
 QY 422 AGCTGGCCACGATATCACTATTGCGCTTGTGACGTGTCTCTCAAAAAATTGCGAGAAG 481
 Db 361 AGCTGGCCACGATATCACTATTGCGCTTGTGACGTGTCTCTCAAAAAATTGCGAGAAG 420
 QY 482 TGGTGAGAAATCCGTATGCCCCCGCTGAATCTCCGTGCTGACTTTGCTGTGTGCGCTTAT 541
 Db 421 TGGTGAGAAATCCGTATGCCCCCGCTGAATCTCCGTGCTGACTTTGCTGTGTGCGCTTAT 480
 QY 542 GTGTGACCTGGGCATTTATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGT 601
 Db 481 GTGTGACCTGGGCATTTATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGT 540
 QY 602 CATGTGCAAAATATGCTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCA 661
 Db 541 CATGTGCAAAATATGCTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCA 600
 QY 662 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGATGTTGAGGACCTTT 721
 Db 601 GAAATCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGATGTTGAGGACCTTT 660
 QY 722 CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGAGCAATGAACCCCA 781
 Db 661 CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGAGCAATGAACCCCA 720
 QY 782 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 841
 Db 721 GTTCTACGAGCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 780
 QY 842 GAGCATGATGATGGCCAGAAATGAAGAAGATTGACAGATGATTTGCAAGAAGAC 901
 Db 781 GAGCATGATGATGGCCAGAAATGAAGAAGATTGACAGATGATTTGCAAGAAGAC 840
 QY 902 GAAGCAGAGTGTGTCAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGAC 961
 Db 841 GAAGCAGAGTGTGTCAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGAC 900
 QY 962 TTTTGAGGAGTGTGTTCATCATGATCACAACAAGGAGGCGCTGTTATCACCAGTGA 1021
 Db 901 TTTTGAGGAGTGTGTTCATCATGATCACAACAAGGAGGCGCTGTTATCACCAGTGA 960
 QY 1022 GGAGCAGGAGCTGAGCCCCCGCTGACCTGTGCTGTTAAACACCCAGCCATCCCTTC 1081
 Db 961 GGAGCAGGAGCTGAGCCCCCGCTGACCTGTGCTGTTAAACACCCAGCCATCCCTTC 1020
 QY 1082 TTTCAAAAGGATCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGATTT 1141
 Db 1021 TTTCAAAAGGATCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGATTT 1080
 QY 1142 CAGCCGCGAAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGATAAAGGTAAA 1201
 Db 1081 CAGCCGCGAAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGATAAAGGTAAA 1140
 QY 1202 AGCTAGTCTTAACTTCCAGGCCACGCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1261
 |||||||

Db 1141 AGCTAGTCTTAACTTCCAGGCCACGCGCTCAAGTGAATTTGAATACTGCAATTTACAGTG 1200
 QY 1262 TAGAGTACACATTAACATTTGATGCATGGAACATGAGGAACAGTATTTACAGTGTCTA 1321
 Db 1201 TAGAGTACACATTAACATTTGATGCATGGAACATGAGGAACAGTATTTACAGTGTCTA 1260
 QY 1322 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGATGATGAATTTCTAAA 1381
 Db 1261 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGATGATGAATTTCTAAA 1320
 QY 1382 AATGTTATCATTTAGGCTTTGATTTATAAACTTTGGTACTTATATAAATTATGTT 1441
 Db 1321 AATGTTATCATTTAGGCTTTGATTTATAAACTTTGGTACTTATATAAATTATGTT 1380
 QY 1442 AGTTATTTCTGCCCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTCTGACTTATA 1501
 Db 1381 AGTTATTTCTGCCCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTCTGACTTATA 1440
 QY 1502 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTGAAGACATGATATACATTT 1561
 Db 1441 TTTTGAATGGGTTCTAGTGAAGAAAGAAATGATATTTCTGAAGACATGATATACATTT 1500
 QY 1562 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAATTTGATGGTAT 1621
 Db 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAATGCCACAATTTGATGGTAT 1560
 QY 1622 AAAAGTCACGTGAACAGA 1640
 Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 6
 US-09-232-149A-107
 ; Sequence 107, Application US/09232149A
 ; Patent No. 6465611
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
 ; FILE REFERENCE: 210121.427C6
 ; CURRENT APPLICATION NUMBER: US/09/232,149A
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 107
 ; LENGTH: 1621
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-232-149A-107

Query Match 78.5%; Score 1574.2; DB 4; Length 1621;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 62 CGCCATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCCTGGCCCCGGCCGCTT 121
 Db 1 CGCCATGGCACTGCAGGGCATCTCGTGTGAGCTGTCCGGCCTGGCCCCGGCCGCTT 60
 QY 122 CTGTGCTATGCTCTGCTGCTGACTTCGGGGCGGTGTGTACGCGTGAACCGCCGCTC 181
 Db 61 CTGTGCTATGCTCTGCTGCTGACTTCGGGGCGGTGTGTACGCGTGAACCGCCGCTC 120
 QY 182 CCGCTACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGTAGTGTGAGCTGAAGCA 241
 Db 121 CCGCTACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGTAGTGTGAGCTGAAGCA 180
 QY 242 GCCCGGGGAGCCCGCTGCTGCGGCGTGTGCAAGCGGTGAGATGCTGCTGAGGCC 301
 Db 181 GCCCGGGGAGCCCGCTGCTGCGGCGTGTGCAAGCGGTGAGATGCTGCTGAGGCC 240
 QY 302 CTTCGGCGCGGTGTGATGGAGAACTCAGCTGGGCCAGAGATTCTGACGGGAAAA 361

|||||
Db 241 CTCGCCCGCGGTGCATGAGAACTCCAGCTGGCCCCAGAGATTCTGCAGCGGAAAA 300
QY 362 TCCAAGCCTATTATGCGCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCGGGT 421
Db 301 TCCAAGCCTATTATGCGCAGGCTGAGTGATTTGGCCAGTCAGGAAGCTTCTGCGGGT 360
QY 422 AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAG 481
Db 361 AGCTGGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAG 420
QY 482 TGGTGAGAAATCCGTATGCCCGCTGAATCTCCGTGCTGACTTTGCTGCTGCTGCTTAT 541
Db 421 TGGTGAGAAATCCGTATGCCCGCTGAATCTCCGTGCTGACTTTGCTGCTGCTGCTTAT 480
QY 542 GTGTGCACCTGGGCAATTATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGGTCAGT 601
Db 481 GTGTGCACCTGGGCAATTATATGGCTCTTTTGAACCGCACACGCACTGGCAAGGGTCAGT 540
QY 602 CATTCATGCAAAATATGTTGGAGAACAACAGCATTTTAAGTCTTTTCTGTGAAAACTCA 661
Db 541 CATTCATGCAAAATATGTTGGAGAACAACAGCATTTTAAGTCTTTTCTGTGAAAACTCA 600
QY 662 GAAATCGAGTCTGTGGGAGACACCTCGAGACAGAACATGTTGGATGGTGAGCACCTTT 721
Db 601 GAAATCGAGTCTGTGGGAGACACCTCGAGACAGAACATGTTGGATGGTGAGCACCTTT 660
QY 722 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCCA 781
Db 661 CTATACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCCA 720
QY 782 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 841
Db 721 GTTCTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGAT 780
QY 842 GAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATATTGCAAGAAGAC 901
Db 781 GAGCATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATATTGCAAGAAGAC 840
QY 902 GAAGGCAGAGTGTCTCAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC 961
Db 841 GAAGGCAGAGTGTCTCAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGAC 900
QY 962 TTTTGAGGAGTGTCTCATCATGATCACAACAAGAAAGGGGCTGTTTATCACCAGTGA 1021
Db 901 TTTTGAGGAGTGTCTCATCATGATCACAACAAGAAAGGGGCTGTTTATCACCAGTGA 960
QY 1022 GGAGCAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1081
Db 961 GGAGCAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
QY 1082 TTTCAAAAAGGATCCCTTCATAGAGAAACACACATGAGAGATACTTGAAGATTGGATT 1141
Db 1021 TTTCAAAAAGGATCCCTTCATAGAGAAACACACATGAGAGATACTTGAAGATTGGATT 1080
QY 1142 CAGCCGCGAAGAGATTATCAGCTTAAGTAAATCATGAAAGTAATTAAGSTAAA 1201
Db 1081 CAGCCGCGAAGAGATTATCAGCTTAAGTAAATCATGAAAGTAATTAAGSTAAA 1140
QY 1202 AGCTAGTCTTAAGTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTCAAGTG 1261
Db 1141 AGCTAGTCTTAAGTCCAGGCCCCAGGCTCAAGTGAATTTGAATTAAGTCAAGTG 1200
QY 1262 TAGAGTAACACATTAACATTTGATGCATGGAACATGAGAGACAGTATTACAGTCTCCTA 1321
Db 1201 TAGAGTAACACATTAACATTTGATGCATGGAACATGAGAGACAGTATTACAGTCTCCTA 1260
QY 1322 CCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAAA 1381
Db 1261 CCACTCTAATCAAGAAAAGAAATTAACAGACTCTGATTTCTACAGTGAATTTCTAAA 1320
QY 1382 AATGCTTATCATAGGGCTTTTGATTTATAAACTTTGGGTACTTATCTAAATTTATGGT 1441
|||||

Db 1321 AATGCTTATCATAGGGCTTTTGATTTATAAACTTTGGGTACTTATACTAAATTATGGT 1380
QY 1442 AGTATATTCGCTTCCAGATTTGCTTGATTAATTTGTTGATTAATTAAGATTTGACTTATA 1501
Db 1381 AGTATATTCGCTTCCAGATTTGCTTGATTAATTTGTTGATTAATTAAGATTTGACTTATA 1440
QY 1502 TTTTGAATGGGTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1561
Db 1441 TTTTGAATGGGTCTAGTGAAGAAAGATGATATATTTCTTGAAGACATCGATATACATTT 1500
QY 1562 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAAATGCCAATAATTGTATGTGAT 1621
Db 1501 ATTTACACTCTTGATTTCTACAATGTAGAAAATGAGAAAATGCCAATAATTGTATGTGAT 1560
QY 1622 AAAAGTCACGTGAACAGA 1640
Db 1561 AAAAGTCACGTGAACAAA 1579

RESULT 7
US-09-020-956-74
; Sequence 74, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillin, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-74

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred.No.3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTCATAGGAGAACACACTAGGAGATCTTGAAGAATTGGATTTCAGCGCGGAAGAGAT 1156
Db 1 TTTCATAGGAGAACACACTAGGAGATCTTGAAGAATTGGATTTCAGCGCGGAAGAGAT 60
QY 1157 TTATCAGCTTAACATCAGATTAATCATTTGAAGTAATAAGGTAAGGTAAGCTTCTTAAT 1216
Db 61 TTATCAGCTTAACATCAGATTAATCATTTGAAGTAATAAGGTAAGGTAAGGTAAGCTTCTTAAT 120

```

QY 1217 TCCAGGCCACGGCTCAAGTGAATTGAACTACTGCATTACAGTGTAGAGTAACACATAA 1276
Db 121 TCCAGGCCACGGCTCAAGTGAATTGAACTACTGCATTACAGTGTAGAGTAACACATAA 180
QY 1277 CATGTATGCATGGAACATGAGAGACACAGTATTTACAGTGTCTTACCACTCTAATCAAGA 1336
Db 181 CATGTATGCATGGAACATGAGAGACAGTATTTACAGTGTCTTACCACTCTAATCAAGA 240
QY 1337 AAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAATAAGTGTATCATTA 1396
Db 241 AAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAATAAGTGTATCATTA 300
QY 1397 GGCCTTTGATTTATAAACTTTGGGCTACTTATTAATAATTAAGTGTATTTCTGCTTC 1456
Db 301 GGCCTTTGATTTATAAACTTTGGGCTACTTATTAATAATTAAGTGTATTTCTGCTTC 360
QY 1457 CAGTTTCTGATATATTTGTTGATTTAAGATTTCTGACTTATTTGAATGGTTC 1516
Db 361 CAGTTTCTGATATATTTGTTGATTTAAGATTTCTGACTTATTTGAATGGTTC 420
QY 1517 AGTGAAGAAGCATGATATATTTCTGAAGACATCGATATACATTTATTTACACTCTTGAT 1576
Db 421 ACTGAAGAAGCATGATATATTTCTGAAGACATCGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAATG-AGGAATGCCACAATTTGATGTTGATTAAGTCACGT 1632
Db 481 TCTACAATGTAGAAATGAGGAATGCCCAATTTGATGTTGATTAAGTCACGT 537

```

RESULT 8
US-09-030-607-74
Sequence 74, Application US/09030607
Patent No. 6262245

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607

FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 537 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORGANISM: Homo sapiens

US-09-030-607-74

```

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTTCATAGAGAGAACACACTGAGGAGACTTGAAGAAATTTGGATTTCAGCCGGAAGAGAT 1156
Db 1 TTTTCATAGAGAGAACACACTGAGGAGACTTGAAGAAATTTGGATTTCAGCCGGAAGAGAT 60
QY 1157 TTATCAGCTTAACCTCAGATAAATATCTGAAAGTAAATGAAGTAAAGCTAGTCTTAAC 1216
Db 61 TTATCAGCTTAACCTCAGATAAATATCTGAAAGTAAATGAAGTAAAGCTAGTCTTAAC 120
QY 1217 TCCAGGCCACGGCTCAAGTGAATTGAACTACTGCATTACAGTGTAGAGTAACACATAA 1276
Db 121 TCCAGGCCACGGCTCAAGTGAATTGAACTACTGCATTACAGTGTAGAGTAACACATAA 180
QY 1277 CATGTATGCATGGAACATGAGAGACAGTATTTACAGTGTCTTACCACTCTAATCAAGA 1336
Db 181 CATGTATGCATGGAACATGAGAGACAGTATTTACAGTGTCTTACCACTCTAATCAAGA 240
QY 1337 AAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAATAAGTGTATCATTA 1396
Db 241 AAAGAAATTACAGACTCTGATTTCTACAGTGTGATTTGAATTTCTAAATAAGTGTATCATTA 300
QY 1397 GGCCTTTGATTTATAAACTTTGGGCTACTTATTAATAATTAAGTGTATTTCTGCTTC 1456
Db 301 GGCCTTTGATTTATAAACTTTGGGCTACTTATTAATAATTAAGTGTATTTCTGCTTC 360
QY 1457 CAGTTTCTGATATATTTGTTGATTTAAGATTTCTGACTTATTTGAATGGTTC 1516
Db 361 CAGTTTCTGATATATTTGTTGATTTAAGATTTCTGACTTATTTGAATGGTTC 420
QY 1517 AGTGAAGAAGCATGATATATTTCTGAAGACATCGATATACATTTATTTACACTCTTGAT 1576
Db 421 ACTGAAGAAGCATGATATATTTCTGAAGACATCGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAATG-AGGAATGCCACAATTTGATGTTGATTAAGTCACGT 1632
Db 481 TCTACAATGTAGAAATGAGGAATGCCCAATTTGATGTTGATTAAGTCACGT 537

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RESULT 9
US-09-605-785-74
Sequence 74, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolck, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darriek

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C16

CURRENT APPLICATION NUMBER: US/09/605,785

CURRENT FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 835

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 74

LENGTH: 537

TYPE: DNA


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; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(537)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-74

```

```

Query Match      25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```

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QY 1097 TTTCATAGGAGAACACACTGAGAGATCTTGAAGAATTGGATTCAGCCCGGAGAGAT 1156
    |||
Db 1 TTTCATAGGAGAACACACTGAGAGATCTTGAAGAATTGGATTCAGCCCGGAGAGAT 60
QY 1157 TTATCAGCTTAACCTCAGATAAATCAATTGAAAGTAAGTAAAGCTAGTCTTAAC 1216
    |||
Db 61 TTATCAGCTTAACCTCAGATAAATCAATTGAAAGTAAGTAAAGCTAGTCTTAAC 120
QY 1217 TCCAGGCCACGGCTCAAGTGAATTGAACTGCACTTTACAGTGTAGAGTAACACATAA 1276
    |||
Db 121 TCCAGGCCACGGCTCAAGTGAATTGAACTGCACTTTACAGTGTAGAGTAACACATAA 180
QY 1277 CATGTATGCATGGAACATGAGAGACAGTATTACAGTGTCTTACCCTCTAATCAAGA 1336
    |||
Db 181 CATGTATGCATGGAACATGAGAGACAGTATTACAGTGTCTTACCCTCTAATCAAGA 240
QY 1337 AAAGAATTACAGACTCTGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT 1396
    |||
Db 241 AAAGAATTACAGACTCTGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT 300
QY 1397 GGCTTTGATTTATAAACTTTGGGTACTTATACATAATATGATGATGATGATGATGAT 1456
    |||
Db 301 GGCTTTGATTTATAAACTTTGGGTACTTATACATAATATGATGATGATGATGATGAT 360
QY 1457 CAGTTTGCTGATATATTTGTTGATATTAAGATCTTGACCTTATATTTGAATGGTCT 1516
    |||
Db 361 CAGTTTGCTGATATATTTGTTGATATTAAGATCTTGACCTTATATTTGAATGGTCT 420
QY 1517 AGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTTATTTACACTCTTGAT 1576
    |||
Db 421 ACTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAAATG-AGGAAATGCCCAAAATGTGATGATGATGATGATGAT 1632
    |||
Db 481 TCTACAATGTAGAAAATGAGGAAATGCCCAAAATGTGATGATGATGATGATGATGAT 537

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RESULT 10
US-09-439-313-74
; Sequence 74, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(537)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-74

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```

Query Match      25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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QY 1097 TTTCATAGGAGAACACACTGAGAGATCTTGAAGAATTGGATTCAGCCCGGAGAGAT 1156
    |||
Db 1 TTTCATAGGAGAACACACTGAGAGATCTTGAAGAATTGGATTCAGCCCGGAGAGAT 60
QY 1157 TTATCAGCTTAACCTCAGATAAATCAATTGAAAGTAAGTAAAGCTAGTCTTAAC 1216
    |||
Db 61 TTATCAGCTTAACCTCAGATAAATCAATTGAAAGTAAGTAAAGCTAGTCTTAAC 120
QY 1217 TCCAGGCCACGGCTCAAGTGAATTGAACTGCACTTTACAGTGTAGAGTAACACATAA 1276
    |||
Db 121 TCCAGGCCACGGCTCAAGTGAATTGAACTGCACTTTACAGTGTAGAGTAACACATAA 180
QY 1277 CATGTATGCATGGAACATGAGAGACAGTATTACAGTGTCTTACCCTCTAATCAAGA 1336
    |||
Db 181 CATGTATGCATGGAACATGAGAGACAGTATTACAGTGTCTTACCCTCTAATCAAGA 240
QY 1337 AAAGAATTACAGACTCTGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT 1396
    |||
Db 241 AAAGAATTACAGACTCTGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT 300
QY 1397 GGCTTTGATTTATAAACTTTGGGTACTTATACATAATATGATGATGATGATGATGAT 1456
    |||
Db 301 GGCTTTGATTTATAAACTTTGGGTACTTATACATAATATGATGATGATGATGATGAT 360
QY 1457 CAGTTTGCTGATATATTTGTTGATATTAAGATCTTGACCTTATATTTGAATGGTCT 1516
    |||
Db 361 CAGTTTGCTGATATATTTGTTGATATTAAGATCTTGACCTTATATTTGAATGGTCT 420
QY 1517 AGTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTTATTTACACTCTTGAT 1576
    |||
Db 421 ACTGAAGAAAGATGATATTTCTTGAAGACATCGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAAATG-AGGAAATGCCCAAAATGTGATGATGATGATGATGAT 1632
    |||
Db 481 TCTACAATGTAGAAAATGAGGAAATGCCCAAAATGTGATGATGATGATGATGATGAT 537

```

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RESULT 11
US-09-352-616A-74
; Sequence 74, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(537)

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; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-74

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTCATAGAGACACACTGAGAGATCTGAGAAATTGGATTACGCCCGGAGAGAT 1156
|||||
Db 1 TTTCATAGAGACACACTGAGAGATCTGAGAAATTGGATTACGCCCGGAGAGAT 60
QY 1157 TTATCAGCTTAACCTAGATATAAATCATTTGAAGTAATAAGCTAGTCTTAAT 1216
|||||
Db 61 TTATCAGCTTAACCTAGATATAAATCATTTGAAGTAATAAGCTAGTCTTAAT 120
QY 1217 TCCAGGCCACGGCTCAAGTGAATTGGAATCTGATTTACAGTGTAGAGTAACATTA 1276
|||||
Db 121 TCCAGGCCACGGCTCAAGTGAATTGGAATCTGATTTACAGTGTAGAGTAACATTA 180
QY 1277 CATTTGATGATGAACATGAGGAACAGTATTAAGTGTCTTACACCTCTAATCAAGA 1336
|||||
Db 181 CATTTGATGATGAACATGAGGAACAGTATTAAGTGTCTTACACCTCTAATCAAGA 240
QY 1337 AAAGAATTACAGACTCTGATCTTACAGTGAATGTAATCTAAAAATGGTTATCATTA 1396
|||||
Db 241 AAAGAATTACAGACTCTGATCTTACAGTGAATGTAATCTAAAAATGGTTATCATTA 300
QY 1397 GGCTTTGATTTATTAACCTTTGGTACTTATCTAAATTATGATGATTTGCTTTC 1456
|||||
Db 301 GGCTTTGATTTATTAACCTTTGGTACTTATCTAAATTATGATGATTTGCTTTC 360
QY 1457 CAGTTGCTGATATATTTGTTGATATTAAGATCTTGACTATATTTGAATGGGTTCT 1516
|||||
Db 361 CAGTTGCTGATATATTTGTTGATATTAAGATCTTGACTATATTTGAATGGGTTCT 420
QY 1517 AGTGAAGGAATGATATATTTCTTGAAGACATGATATACATTTATTTACACTCTTGAT 1576
|||||
Db 421 ACTGAAAAAANGAATGATATATTTCTTGAAGACATGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAAAATG-AGGAATGCCACAAATTGTATGTTGATTAAGTCACGT 1632
|||||
Db 481 TCTACAATGTAGAAAAATGAAAGAAATGCCCAATTGTATGTTGATTAAGTCACGT 537

RESULT 12
US-09-232-149A-74
; Sequence 74, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(537)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-74

Query Match 25.7%; Score 515; DB 4; Length 537;
Best Local Similarity 98.5%; Pred. No. 3.8e-136;
Matches 529; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1097 TTTCATAGAGACACACTGAGAGATCTGAGAAATTGGATTACGCCCGGAGAGAT 1156
|||||
Db 1 TTTCATAGAGACACACTGAGAGATCTGAGAAATTGGATTACGCCCGGAGAGAT 60
QY 1157 TTATCAGCTTAACCTAGATATAAATCATTTGAAGTAATAAGCTAGTCTTAAT 1216
|||||
Db 61 TTATCAGCTTAACCTAGATATAAATCATTTGAAGTAATAAGCTAGTCTTAAT 120
QY 1217 TCCAGGCCACGGCTCAAGTGAATTGGAATCTGATTTACAGTGTAGAGTAACATTA 1276
|||||
Db 121 TCCAGGCCACGGCTCAAGTGAATTGGAATCTGATTTACAGTGTAGAGTAACATTA 180
QY 1277 CATTTGATGATGAACATGAGGAACAGTATTAAGTGTCTTACACCTCTAATCAAGA 1336
|||||
Db 181 CATTTGATGATGAACATGAGGAACAGTATTAAGTGTCTTACACCTCTAATCAAGA 240
QY 1337 AAAGAATTACAGACTCTGATCTTACAGTGAATGTAATCTAAAAATGGTTATCATTA 1396
|||||
Db 241 AAAGAATTACAGACTCTGATCTTACAGTGAATGTAATCTAAAAATGGTTATCATTA 300
QY 1397 GGCTTTGATTTATTAACCTTTGGTACTTATCTAAATTATGATGATTTGCTTTC 1456
|||||
Db 301 GGCTTTGATTTATTAACCTTTGGTACTTATCTAAATTATGATGATTTGCTTTC 360
QY 1457 CAGTTGCTGATATATTTGTTGATATTAAGATCTTGACTATATTTGAATGGGTTCT 1516
|||||
Db 361 CAGTTGCTGATATATTTGTTGATATTAAGATCTTGACTATATTTGAATGGGTTCT 420
QY 1517 AGTGAAGGAATGATATATTTCTTGAAGACATGATATACATTTATTTACACTCTTGAT 1576
|||||
Db 421 ACTGAAAAAANGAATGATATATTTCTTGAAGACATGATATACATTTATTTACACTCTTGAT 480
QY 1577 TCTACAATGTAGAAAAATG-AGGAATGCCACAAATTGTATGTTGATTAAGTCACGT 1632
|||||
Db 481 TCTACAATGTAGAAAAATGAAAGAAATGCCCAATTGTATGTTGATTAAGTCACGT 537

RESULT 13
US-09-020-956-3/c
; Sequence 3, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-020-956-3

Query Match 20.3%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 2.4e-105;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 676 GGAAGCACCCTCGAGACAGACATGTTGGATGTTGAGCACCCTTCTATAGACTTACA 735
DB 415 GGGCCCCCCTCGAGACAGACATGTTGGATGTTGAGCACCCTTCTATAGACTTACA 356
QY 736 GGACAGCAGATGGGAATTGCTGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 795
DB 355 GGACAGCAGATGGGAATTGCTGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 296
QY 796 TGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATT 855
DB 295 TGATCAAGGANNTTGACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATT 236
QY 856 GGCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAGCAGAGTGT 915
DB 235 GGCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAGCAGAGTGT 176
QY 916 GTCAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 975
DB 175 GTCAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 116
QY 976 TTCATCATGATCACAACAGGAAGCGGGCTCTTATCACCAGTGAGAGCAGAGCTGA 1035
DB 115 TTCATCATGATCACAACAGGAAGCGGGCTCTTATCACCAGTGAGAGCAGAGCTGA 56
QY 1036 GCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1090
DB 55 GCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1

RESULT 14
US-09-030-607-3/c
Sequence 3, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-3

Query Match 20.3%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 2.4e-105;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 676 GGAAGCACCCTCGAGCAGACATGTTGGATGTTGAGCACCCTTCTATAGACTTACA 735
DB 415 GGGCCCCCCTCGAGCAGACATGTTGGATGTTGAGCACCCTTCTATAGACTTACA 356
QY 736 GGACAGCAGATGGGAATTGCTGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 795
DB 355 GGACAGCAGATGGGAATTGCTGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGC 296
QY 796 TGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATT 855
DB 295 TGATCAAGGANNTTGACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATT 236
QY 856 GGCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAGCAGAGTGT 915
DB 235 GGCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAGCAGAGTGT 176
QY 916 GTCAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 975
DB 175 GTCAATCTTTGACGGCAGAGATGCTGTGTGACTCCGGTCTGACTTTTGAGGAGTTG 116
QY 976 TTCATCATGATCACAACAGGAAGCGGGCTCTTATCACCAGTGAGAGCAGAGCTGA 1035
DB 115 TTCATCATGATCACAACAGGAAGCGGGCTCTTATCACCAGTGAGAGCAGAGCTGA 56
QY 1036 GCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1090
DB 55 GCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAG 1

RESULT 15
US-09-605-785-3/c
Sequence 3, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/605,785
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 773
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)...(773)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-3
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Query Match      20.3%; Score 406.6; DB 4; Length 773;
Best Local Similarity 98.6%; Pred. No. 2.4e-105;
Matches 409; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 415 GGGCCCCCTCGAGACAGACATGTTGATGGTGGAGCACCTTCTATACGACTTACA 356

QY 736 GGACAGCAGATGGGGAATTGCTGCTGTGGAGCAATAGAACCCAGTTCTACGAGCTGC 795
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QY 1036 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAAG 1090
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Db 55 GGGGGGGGGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTCAAAAG 1
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Search completed: April 2, 2003, 02:24:55
Job time : 89.9924 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on:      April 1, 2003, 18:34:28 ; Search time 493.773 Seconds
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Title:	US-09-967-305-1
Perfect score:	2005
Sequence:	1 ttgcagcgtcgtggtcgg.....acatccagaataaagttct 2005

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      2185239 segs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478
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Minimum DB seq length: 0
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Post-processing:	Minimum Match 0%
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	Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2005	100.0	2005	24	AAD38603	Human alpha-methyl
2	2003.4	99.9	2005	24	AAD38607	Human alpha-methyl
3	2003.4	99.9	2069	24	AAD38604	Human alpha-methyl
4	1998.6	99.7	2376	23	ABV21293	Human prostate exp
5	1998.6	99.7	2376	23	ABV21881	Human prostate exp
6	1998.6	99.7	2376	23	ABV25239	Human prostate exp
7	1998.6	99.7	2376	23	ABV27112	Human prostate exp
8	1950.8	97.3	2068	24	ABK92152	Prostate cancer-as
9	1671.4	83.4	3023	24	AAD38606	Human alpha-methyl

10	1653.2	82.5	1674	22	AAH13696	Human CDNA sequenc
11	1574.2	78.5	1621	19	AAV61199	Full length CDNA s
12	1574.2	78.5	1621	19	AAV58584	Prostate tumour sp
13	1574.2	78.5	1621	21	AAA06347	Human Immunogenic
14	1574.2	78.5	1621	22	AAS63555	Human prostate CDN
15	1574.2	78.5	1621	22	AAS10106	Human prostate tum
16	1574.2	78.5	1621	22	AAH93463	Human prostate-spe
17	1574.2	78.5	1621	22	AAH84777	Human prostate-spe
18	1574.2	78.5	1621	22	AAH02528	Prostate tumour an
19	1574.2	78.5	1621	24	ABL94927	Human F1-12 CDNA s
20	1197	59.7	3654	24	AAD38605	Human alpha-methyl
21	997.8	49.8	1039	22	AAC91303	Human polynucleoti
22	905.2	45.1	1294	23	ABV22620	Human prostate exp
23	905.2	45.1	1294	23	ABV22733	Human prostate exp
24	905.2	45.1	1294	23	ABV27711	Human prostate exp
25	905.2	45.1	1294	23	ABV28442	Human prostate exp
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27	830	41.4	1504	24	ABK63669	Rat sequence diffe
28	804	40.1	1317	22	AAH17637	Human CDNA sequenc
29	685.8	34.2	720	22	AAH03341	Human CDNA clone (
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34	594.8	29.7	865	23	ABV28711	Human prostate exp
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ALIGNMENTS

RESULT 1
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ID AAD38603 standard; cDNA; 2005 BP.

DT 23-SEP-2002 (first entry)

Human alpha-methylacyl-CoA racemase SV1 cDNA #1.

KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;

KW cytostatic; SV1; gene; ss-

XX

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	66..1214

FT	/product= "Human SV1 protein #1"
FT	/note= "This region is specifically claimed as
FT	SEQ ID NO: 3 in claim 54 of the specification"

PN WO200227324-A2.

PD 04-APR-2002.

PF 28-SEP-2001; 2001WO-US30532.

PR 28-SEP-2000; 2000US-236238P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23971.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase -
PS
PS Claim 54; Fig 1; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer, e.g. prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase SV1 cDNA.
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SQ Sequence 2005 BP; 519 A; 427 C; 514 G; 545 T; 0 other;

Query Match 100.0%; Score 2005; DB 24; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1981 CAGCAACATCCAGAAATTAAGTTCT 2005
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Db 1981 CAGCAACATCCAGAAATTAAGTTCT 2005

RESULT 2
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AC AAD38607;
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DT 23-SEP-2002 (first entry)
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DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.
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KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
XX cytosolic; SV4; gene; ss.
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OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 66..1214
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FT /product= "Human SV4 protein"

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PN WO200227324-A2.
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PD 04-APR-2002.
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PF 28-SEP-2001; 2001WO-US30532.
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PR 28-SEP-2000; 2000US-236238P.
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PA (MILL-) MILLENNIUM PHARM INC.
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PI Richardson J, Monahan J;
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DR WPI; 2002-405070/43.
DR P-PSDB; AAE23975.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase -
XX
PS Claim 54; Fig 9; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer, e.g. prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase splice variant, SV4 cDNA.
XX
SQ Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 other;

Query Match 99.9%; Score 2003.4; DB 24; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1501 ATTTTGAATGGTCTCTAGTGAAGAAAGAAATGATATTTCTTGAAGACATCGATATACAT 1560
Db 1501 ATTTTGAATGGTCTCTAGTGAAGAAAGAAATGATATTTCTTGAAGACATCGATATACAT 1560
QY 1561 TATTTACACTCTTGATTTCTACAATGTAGAAATGAGAAATGCCACAAATTTGATGCTGA 1620
Db 1561 TATTTACACTCTTGATTTCTACAATGTAGAAATGAGAAATGCCACAAATTTGATGCTGA 1620
QY 1621 TAAAAGTCACGTGAAGACAGATGATTTGGTTCATCCAGGCCCTTTGCTTGGTGTTCATG 1680
Db 1621 TAAAAGTCACGTGAAGACAGATGATTTGGTTCATCCAGGCCCTTTGCTTGGTGTTCATG 1680
QY 1681 ATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGCTTATCACACTTTGTAATTTGCAA 1740
Db 1681 ATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGCTTATCACACTTTGTAATTTGCAA 1740
QY 1741 GAAAAGTTTCACCTGTATTTGAATCAGAATGCTTCAACTGAAAAAACAATATCCAAAAATA 1800
Db 1741 GAAAAGTTTCACCTGTATTTGAATCAGAATGCTTCAACTGAAAAAACAATATCCAAAAATA 1800
QY 1801 ATGAGGAATGTGTGGCTCACTACGTAGAGTCAGAGGGACAGTCACTTTAGGGTTGC 1860
Db 1801 ATGAGGAATGTGTGGCTCACTACGTAGAGTCAGAGGGACAGTCACTTTAGGGTTGC 1860
QY 1861 CTGTATCCAGTAACCTCGGGCCCTGTTCCCGGTGGTCTCTGGGCTGTCAAGCTTTCTTT 1920
Db 1861 CTGTATCCAGTAACCTCGGGCCCTGTTCCCGGTGGTCTCTGGGCTGTCAAGCTTTCTTT 1920
QY 1921 CTCCATGTGTGATTTCTCTCCTCAGGCTGTAGCAAGTTCTGGATCTTATACCAACACA 1980
Db 1921 CTCCATGTGTGATTTCTCTCCTCAGGCTGTAGCAAGTTCTGGATCTTATACCAACACA 1980
QY 1981 CAGCAACATCCAGAAATAAAGTTCT 2005
Db 1981 CAGCAACATCCAGAAATAAAGATCT 2005

RESULT 3
AAD38604
ID AAD38604 standard; cDNA; 2069 BP.
XX
AC AAD38604;
XX
DT 23-SEP-2002 (first entry)

XX DE Human alpha-methylacyl-CoA racemase SV1 cDNA #2.
XX KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW cytostatic; SV1; gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 90..1238
FT FT /*tag= a
FT FT /product= "Human SV1 protein #2"
XX
PN WO200227324-A2.
XX
XX PD 04-APR-2002.
XX PF 28-SEP-2001; 2001WO-US30532.
XX PR 28-SEP-2000; 2000US-236238P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Richardson J, Monahan J;
XX DR WPI: 2002-405070/43.
DR P-PSDB; AAE23972.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase
XX
XX Claim 54; Fig 3; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer, e.g., prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase SV1 cDNA.
XX
SQ Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 other;

Query Match 99.9%; Score 2003.4; DB 24; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2004; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCTTCAAGCGGGCACTGGGAA 60
Db 25 TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCTTCAAGCGGGCACTGGGAA 84
QY 61 GCGCCATGGCAGTGCAGGGCATCTCGGTCTGAGACTGTCCGGCTGGCCCGGCCCGCT 120
Db 85 GCGCCATGGCAGTGCAGGGCATCTCGGTCTGAGACTGTCCGGCTGGCCCGGCCCGCT 144
QY 121 TCTGTCTATGTCCTGCTGACTTCCGGGGCGCTGTGTGTAAGCGGTGAGACCGCCCGCT 180
Db 145 TCTGTCTATGTCCTGCTGACTTCCGGGGCGCTGTGTGTAAGCGGTGAGACCGCCCGCT 204
QY 181 CCCGCTACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 240
Db 205 CCCGCTACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 264
QY 241 AGCCGGGGGAGCCCGCTGCTGCGGCTCTGTGCAAGCGGTGAGATGTGCTGTGAGC 300
Db 265 AGCCGGGGGAGCCCGCTGCTGCGGCTCTGTGCAAGCGGTGAGATGTGCTGTGAGC 324
QY 301 CCTTCCGCGCGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTTCTGACCGGGGAAA 360
Db 325 CCTTCCGCGCGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTTCTGACCGGGGAAA 384

QY 361 ATCCAAGCCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGT 420
Db 385 ATCCAAGCCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGT 444
QY 421 TAGCTGGCCAGCATATCAACTATTGGCTTTGTCAGGCTTCTCTCAAAAATTGGCAGAA 480
Db 445 TAGCTGGCCAGCATATCAACTATTGGCTTTGTCAGGCTTCTCTCAAAAATTGGCAGAA 504
QY 481 GTGTGAGAAATCCGATATGCCCCGCTGAATCTCTGCTGACTTTGCTGTGGTGGCCCTTA 540
Db 505 GTGTGAGAAATCCGATATGCCCCGCTGAATCTCTGCTGACTTTGCTGTGGTGGCCCTTA 564
QY 541 TGTGTGCACTGGGCATTTAATGCGCTTTTGGACCCGACACGCACTGGCAAGGCTCAGG 600
Db 565 TGTGTGCACTGGGCATTTAATGCGCTTTTGGACCCGACACGCACTGGCAAGGCTCAGG 624
QY 601 TCATTGATGCAAAATATGCTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTC 660
Db 625 TCATTGATGCAAAATATGCTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTC 684
QY 661 AGAAATCGAGCTCTGTGGGAAGCACCTCGAGAGACAGAACAATGTTGGATGGTGGACACCTT 720
Db 685 AGAAATCGAGCTCTGTGGGAAGCACCTCGAGAGACAGAACAATGTTGGATGGTGGACACCTT 744
QY 721 TCTATACGACTTACAGAGACAGATGGGGAATTCAATGCTGTTGAGCAATAGAACCCT 780
Db 745 TCTATACGACTTACAGAGACAGATGGGGAATTCAATGCTGTTGAGCAATAGAACCCT 804
QY 781 AGTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 840
Db 805 AGTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 864
QY 841 TGAGCATGATGATTTGGCCAGAATAAGAGAAGAGTTTGAGATGTAATTTGCCAAGAAGA 900
Db 865 TGAGCATGATGATTTGGCCAGAATAAGAGAAGAGTTTGAGATGTAATTTGCCAAGAAGA 924
QY 901 CGAAGGCAGAGTGTGTCAAACTTTTGAGGCGCACAGATGCTGTGACTCCGGTTCTGA 960
Db 925 CGAAGGCAGAGTGTGTCAAACTTTTGAGGCGCACAGATGCTGTGACTCCGGTTCTGA 984
QY 961 CTTTGAGAGAGTGTTCATCATGATCACAACAAGGAAGGGGCTCGTTTATCACCAGATG 1020
Db 985 CTTTGAGAGAGTGTTCATCATGATCACAACAAGGAAGGGGCTCGTTTATCACCAGATG 1044
QY 1021 AGGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTTAAACACCCCGCATCCCTT 1080
Db 1045 AGGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTTAAACACCCCGCATCCCTT 1104
QY 1081 CTTTCAAAAAGGGATCCCTTTCATAGGAGAAACACACTGAGAGAGATACCTTGAAGAATTGGAT 1140
Db 1105 CTTTCAAAAAGGGATCCCTTTCATAGGAGAAACACACTGAGAGAGATACCTTGAAGAATTGGAT 1164
QY 1141 TCAGCCGCGAAGAGATTTATCAGCTTAAGTCAAGTAAATTCATTGAAGAATAAGGTAA 1200
Db 1165 TCAGCCGCGAAGAGATTTATCAGCTTAAGTCAAGTAAATTCATTGAAGAATAAGGTAA 1224
QY 1201 AAGCTAGTCTCTAAGTTCAGGCCCCCAGCGCTCAAGTGAATTGGAATGTCATTACAGT 1260
Db 1225 AAGCTAGTCTCTAAGTTCAGGCCCCCAGCGCTCAAGTGAATTGGAATGTCATTACAGT 1284
QY 1261 GTAGAGTACACATTAACATTTGATGCATGGAACATGGAAGAACAGTATTACAGTGTCTT 1320
Db 1285 GTAGAGTACACATTAACATTTGATGCATGGAACATGGAAGAACAGTATTACAGTGTCTT 1344
QY 1321 ACCACTCTAATCAAGAAAAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA 1380
Db 1345 ACCACTCTAATCAAGAAAAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA 1404
QY 1381 AAATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATAATTATG 1440
Db 1405 AAATGTTATCATTAGGGCTTTTGAATTAATAAACTTTGGGTACTTATTAATAATTATG 1464

QY 1441 TAGTTATTCCTGCTTCCAGTTTGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTAT 1500
Db 1465 TAGTTATTCCTGCTTCCAGTTTGCTTGATATATTTGTTGATATTAAGATTTCTTGACTTAT 1524
QY 1501 ATTTGAAATGGGTTCTAGTGA AAAAGGAATGATATATTTCTTGAAGACATCGATATACATT 1560
Db 1525 ATTTGAAATGGGTTCTAGTGA AAAAGGAATGATATATTTCTTGAAGACATCGATATACATT 1584
QY 1561 TATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGCTGA 1620
Db 1585 TATTTACACTCTTGATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGCTGA 1644
QY 1621 TAAAAGTCACGTGAACAGAGTGAATGGTTGCATCCAGGCCCTTTGCTTGGTGTTCATG 1680
Db 1645 TAAAAGTCACGTGAACAGAGTGAATGGTTGCATCCAGGCCCTTTGCTTGGTGTTCATG 1704
QY 1681 ATCTCCCTCTAAGCACATTCGAAACTTTAGCAACACGTTATCACACTTTGTAAATTGCCAAA 1740
Db 1705 ATCTCCCTCTAAGCACATTCGAAACTTTAGCAACACGTTATCACACTTTGTAAATTGCCAAA 1764
QY 1741 GAAAAGTTTCACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAAATA 1800
Db 1765 GAAAAGTTTCACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAAATA 1824
QY 1801 ATGAGGAAATGTGTGGCTCCTACCTAGTAGAGTCCAGAGGGACAGTCAGTGTTTAGGGTTGC 1860
Db 1825 ATGAGGAAATGTGTGGCTCCTACCTAGTAGAGTCCAGAGGGACAGTCAGTGTTTAGGGTTGC 1884
QY 1861 CTGTATTCAGTAACTCGGGGCTGTTCCTCCCGTGGGTCTCTGGGCTGTCAAGTTCCTTT 1920
Db 1885 CTGTATTCAGTAACTCGGGGCTGTTCCTCCCGTGGGTCTCTGGGCTGTCAAGTTCCTTT 1944
QY 1921 CTCCATGTGTTGATTTCTCCTCAGGCTGTAGCAAGTCTTGATCTTATACCAACACA 1980
Db 1945 CTCCATGTGTTGATTTCTCCTCAGGCTGTAGCAAGTCTTGATCTTATACCAACACA 2004
QY 1981 CAGCAACATCCAGAAATAAGTTCT 2005
Db 2005 CAGCAACATCCAGAAATAAGATCT 2029

RESULT 4
ABV21293
ID ABV21293 standard; cdna; 2376 BP.
XX
AC ABV21293;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cdna 21284.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX

DR WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -

XX

PS Claim 1; Page 3532; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX

SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;

Query Match 99.7%; Score 1998.6; DB 23; Length 2376;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGCTGGCTGGGGCTAAGGCTGCTCAGTTTCTTCAGCGGGGCACTGGGAA 60

DB |||||||

DB 36 TTGCAGGCTGCTGGCTGGGGCTAAGGCTGCTCAGTTTCTTCAGCGGGGCACTGGGAA 95

QY 61 GCGCCATGGCACTGACGGGCATCTCGCTGAGCTGTCCGGCCTGGCCCCGGCCGT 120

DB |||||||

DB 96 GCGCCATGGCACTGACGGGCATCTCGCTGAGCTGTCCGGCCTGGCCCCGGCCGT 155

QY 121 TCTGTGCTATGCTGCTGCTGACTTCGCGGGCGCTGTGCTAGCGCTGACCGCGCCGCT 180

DB |||||||

DB 156 TCTGTGCTATGCTGCTGCTGACTTCGCGGGCGCTGTGCTAGCGCTGACCGCGCCGCT 215

QY 181 CCCGCTACGACGTGACCGCCTTGGCGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGC 240

DB |||||||

DB 216 CCCGCTACGACGTGACCGCCTTGGCGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGC 275

QY 241 AGCCGGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 300

DB |||||||

DB 276 AGCCGGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 335

QY 301 CCTTCGCGCGGCTGCTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAAA 360

DB |||||||

DB 336 CCTTCGCGCGGCTGCTGATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAAA 395

QY 361 ATCCAAGGCTTATTTATGCCAGGCTGAGTGATTTGCCAGTCAGGAAGCTTCTGCCGT 420

DB |||||||

DB 396 ATCCAAGGCTTATTTATGCCAGGCTGAGTGATTTGCCAGTCAGGAAGCTTCTGCCGT 455

QY 421 TAGCTGGCCAGCATCACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAA 480

DB |||||||

DB 456 TAGCTGGCCAGCATCACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAA 515

QY 481 GTGGTGAGATCCGTATGCCCGGCTGAATCTCTGCGCTGACTTTGCTGGTGGCCCTTA 540

DB |||||||

DB 516 GTGGTGAGATCCGTATGCCCGGCTGAATCTCTGCGCTGACTTTGCTGGTGGCCCTTA 575

QY 541 TGTGTGCACTGGGCACTTATATGGCTCTTTTGAACCGCACACGCACTGCAAGGGTCAGG 600

DB |||||||

DB 576 TGTGTGCACTGGGCACTTATATGGCTCTTTTGAACCGCACACGCACTGCAAGGGTCAGG 635

QY 601 TCATTGATGCAAAATATGCTGGAAGACAGCATATTAAAGTCTTTCTGTGGAATAACTC 660

DB |||||||

DB 636 TCATTGATGCAAAATATGCTGGAAGACAGCATATTAAAGTCTTTCTGTGGAATAACTC 695

QY 661 AGAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTT 720

DB |||||||

DB 696 AGAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTT 755

QY 721 TCTATACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTGAGCAATAGAACCCC 780

DB |||||||

DB 756 TCTATACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTGAGCAATAGAACCCC 815

QY 781 AGTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGA 840

DB |||||||

DB 816 AGTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGA 875

QY 841 TGAGCATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGA 900

DB |||||||

DB 876 TGAGCATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGA 935

QY 901 CGAAGCAGAGTGTGTCAAATCTTTGACGGGCACAGATGCTGTGACTCCGGTCTGA 960

DB |||||||

DB 936 CGAAGCAGAGTGTGTCAAATCTTTGACGGGCACAGATGCTGTGACTCCGGTCTGA 995

QY 961 CTTTGGAGAGTTGTTTCATCATGATCACAACAAGCAAGCGGCTGTTTATCACCACTG 1020

DB |||||||

DB 996 CTTTGGAGAGTTGTTTCATCATGATCACAACAAGCAAGCGGCTGTTTATCACCACTG 1055

QY 1021 AGGAGCAGAGCTGAGCCCCCGCCCTGCACCTGCTGTAAACACCCCGCATCCCTT 1080

DB |||||||

DB 1056 AGGAGCAGAGCTGAGCCCCCGCCCTGCACCTGCTGTAAACACCCCGCATCCCTT 1115

QY 1081 CTTTCAAAAGGATTCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGGAT 1140

DB |||||||

DB 1116 CTTTCAAAAGGATTCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGATTGGAT 1175

QY 1141 TCAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAAAGGTAA 1200

DB |||||||

DB 1176 TCAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAAAGGTAA 1235

QY 1201 AAGCTAGTCTTAACCTCCAGGCCCGCCAGGCTCAAGTGAATTTGAATACCTGCAATTACAGT 1260

DB |||||||

DB 1236 AAGCTAGTCTTAACCTCCAGGCCCGCCAGGCTCAAGTGAATTTGAATACCTGCAATTACAGT 1295

QY 1261 GTAAGTAACACATTAACATTTGTATGATGAGAAACATGGAAGAACAGTATTAACAGTGTCT 1320

DB |||||||

DB 1296 GTAAGTAACACATTAACATTTGTATGATGAGAAACATGGAAGAACAGTATTAACAGTGTCT 1355

QY 1321 ACCACTCTAATCAAGAAAGAAATTACAGACTGCTGATCTTACAGTATGATGAATTCTTAA 1380

DB |||||||

DB 1356 ACCACTCTAATCAAGAAAGAAATTACAGACTGCTGATCTTACAGTATGATGAATTCTTAA 1415

QY 1381 AAATGGTTATCATTTAGGCTTTTGATTTATAAAACTTTGGTACTTATTAATAATTATGG 1440

DB |||||||

DB 1416 AAATGGTTATCATTTAGGCTTTTGATTTATAAACTTTGGTACTTATTAATAATTATGG 1475

QY 1441 TAGTTATCTGCTCCAGTGTGCTGATATATTTGTTGATATTAAGATCTTGACTTAT 1500

DB |||||||

DB 1476 TAGTTATCTGCTCCAGTGTGCTGATATATTTGTTGATATTAAGATCTTGACTTAT 1535

QY 1501 ATTTGAATGGGTTCTAGTGAAAAAGGAATGATATATCTTGAAGACATGATATACATT 1560

DB |||||||

DB 1536 ATTTGAATGGGTTCTAGTGAAAAAGGAATGATATATCTTGAAGACATGATATACATT 1595

QY 1561 TATTTACACTCTTGATTTCTACATGTAGAAAAATGAGAAATGCCACAAATGTATGTGTA 1620

DB |||||||

DB 1596 TATTTACACTCTTGATTTCTACATGTAGAAAAATGAGAAATGCCACAAATGTATGTGTA 1655

QY 1621 TAAAGTCACGTGAACAGAGTGTGTTGTCATCCAGGCCCTTTGTCTTGGTGTCTATG 1680

DB |||||||

DB 1656 TAAAGTCACGTGAACAGAGTGTGTTGTCATCCAGGCCCTTTGTCTTGGTGTCTATG 1715

QY 1681 ATCTCCCTTAAGCAGATTCCAAACTTTAGCAACAGTATACACACTTTGTAATTGCAAA 1740

DB |||||||

DB 1716 ATCTCCCTTAAGCAGATTCCAAACTTTAGCAACAGTATACACACTTTGTAATTGCAAA 1775

QY 1741 GAAAGTTTCACCTGTATTGAATCAGAAATGCTTCACTGAAAAAACATATCCAAATA 1800
DB 1776 GAAAGTTTCACCTGTATTGAATCAGAAATGCTTCACTGAAAAAACATATCCAAATA 1835
QY 1801 ATGAGGAATGTGTGGCTACCTAGTAGAGTCCAGAGGACAGTACGTTTAAAGGTGC 1860
DB 1836 ATGAGGAATGTGTGGCTACCTAGTAGAGTCCAGAGGACAGTACGTTTAAAGGTGC 1895
QY 1861 CTGTATCCAGTAACCTGGGGCTGTTCCTCCGTGGGTCTCTGGCTGTACGCTTTCCTTT 1920
DB 1896 CTGTATCCAGTAACCTGGGGCTGTTCCTCCGTGGGTCTCTGGCTGTACGCTTTCCTTT 1955
QY 1921 CTCCATGTGTGTGATTCTCTCAGGCTGTAGCAAGTCTTGAGTCTTAACCCAAACACA 1980
DB 1956 CTCCATGTGTGTGATTCTCTCAGGCTGTAGCAAGTCTTGAGTCTTAACCCAAACACA 2015
QY 1981 CAGCAACATCCAGAAATAAAGTTCT 2005
DB 2016 CAGCAACATCCAGAAATAAAGATCT 2040

RESULT 5

ABV21881
ID ABV21881 standard; cDNA; 2376 BP.
AC ABV21881;
XX 13-SEP-2002 (first entry)
DT 13-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 21872.
DE Human prostate expression marker cDNA 21872.
XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO200160860-A2.
PN 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US05171.
PF 17-FEB-2000; 2000US-183319P.
XX 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
PI WPI; 2001-662795/76.
DR Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX Claim 1; Page 3719; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
SQ Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTGACAGCTGCTGGGCTGAAGGCTGCTCAGTTTCTTACAGCGGACCTGGGAA 60
DB 36 TTGACAGCTGCTGGGCTGAAGGCTGCTCAGTTTCTTACAGCGGACCTGGGAA 95
QY 61 GCGCCATGCGACTGCAGGCGATCTCGGTGTGAGCTGTCCGGCCCGCCCGCCGT 120
DB 96 GCGCCATGCGACTGCAGGCGATCTCGGTGTGAGCTGTCCGGCCCGCCCGCCGT 155
QY 121 TCTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 156 TCTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 215
QY 181 CCCGCTACGACGTGAGCCGCTTGGGCGGCGGCAAGCGCTGCTAGTGTGACCTGAAC 240
DB 216 CCCGCTACGACGTGAGCCGCTTGGGCGGCGGCAAGCGCTGCTAGTGTGACCTGAAC 275
QY 241 AGCCGCGGGGAGCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 276 AGCCGCGGGGAGCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 335
QY 301 CCTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 336 CCTCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
QY 361 ATCCAAGGCTTATTATGCGAGGCTGAGTGTGATTTGGCCAGTCAAGAACTTCTGCCG 420
DB 396 ATCCAAGGCTTATTATGCGAGGCTGAGTGTGATTTGGCCAGTCAAGAACTTCTGCCG 455
QY 421 TAGCTGGCCAGCATATCAACTATTGGCTTTGTACAGGTCTCTCAAAAATTGGCAGAA 480
DB 456 TAGCTGGCCAGCATATCAACTATTGGCTTTGTACAGGTCTCTCAAAAATTGGCAGAA 515
QY 481 GTGTGAGATCCGTATGCGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 516 GTGTGAGATCCGTATGCGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTG 575
QY 541 TGTGTGACATGGGCTATTAATGCTCTTTTGTACCGCACACGACACTGGCAAGGTCAAG 600
DB 576 TGTGTGACATGGGCTATTAATGCTCTTTTGTACCGCACACGACACTGGCAAGGTCAAG 635
QY 601 TCATTGATGCAATATATGTGAAGAACACATATTAACTTCTTCTGTGTGAAAACTC 660
DB 636 TCATTGATGCAATATATGTGAAGAACACATATTAACTTCTTCTGTGTGAAAACTC 695
QY 661 AGAATCGAGCTCTGTGGGAGCACCTCGAGACAGACAGATGTTGGATGTTGAGCACCTT 720
DB 696 AGAATCGAGCTCTGTGGGAGCACCTCGAGACAGACAGATGTTGGATGTTGAGCACCTT 755
QY 721 TCTATACGACTTACAGACAGACAGATGGGGAATTCAATGCTGTGAGCAATAGAACCC 780
DB 756 TCTATACGACTTACAGACAGACAGATGGGGAATTCAATGCTGTGAGCAATAGAACCC 815
QY 781 AGTTCTACGAGCTGCTGATCAAAAGACTTGAAGTCTGATGAATCTCCCAATCAGA 840
DB 816 AGTTCTACGAGCTGCTGATCAAAAGACTTGAAGTCTGATGAATCTCCCAATCAGA 875
QY 841 TGAGCATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGATTTGCAAGAAGA 900
DB 876 TGAGCATGATGATTGGCCAGAAATGAAGAAGATTTCAGATGATTTGCAAGAAGA 935
QY 901 CGAAGGACAGTGTGTCAAACTTTTGAAGGCGACAGATGCTGTGACTCCGGTTCTGA 960
DB 936 CGAAGGACAGTGTGTCAAACTTTTGAAGGCGACAGATGCTGTGACTCCGGTTCTGA 995

QY 961 CTTTGTGAGAGGTTGTTCAATCATGATCACAACAAGGAGGCTCGTTTATCAGCAGTG 1020
 Db 996 CTTTGTGAGAGGTTGTTCAATCATGATCACAACAAGGAGGCTCGTTTATCAGCAGTG 1055
 QY 1021 AGGAGCAGGAGCGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 1080
 Db 1056 AGGAGCAGGAGCGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 1115
 QY 1081 CTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGAGATACTTGAAGAATTTGGAT 1140
 Db 1116 CTTTCAAAAGGATCCTTTTCATAGGAGAACACACTGAGAGATACTTGAAGAATTTGGAT 1175
 QY 1141 TCAGCCCGGAAGAGATTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGGTAA 1200
 Db 1176 TCAGCCCGGAAGAGATTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGGTAA 1235
 QY 1201 AAGCTAGTCTTAAGTCTCAGGCCCCCAGGCTCAAGTGAATTTGAATTAAGTCAAGT 1260
 Db 1236 AAGCTAGTCTTAAGTCTCAGGCCCCCAGGCTCAAGTGAATTTGAATTAAGTCAAGT 1295
 QY 1261 GTAGAGTAACACATTAATGTATGATGAAACATGAGGAACAGTATTACAGTCTCT 1320
 Db 1296 GTAGAGTAACACATTAATGTATGATGAAACATGAGGAACAGTATTACAGTCTCT 1355
 QY 1321 ACCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGTATGAAATTTCTAA 1380
 Db 1356 ACCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTGTATGAAATTTCTAA 1415
 QY 1381 AATGGTTATCATTAGGCTTTGATTTATAAAACCTTGGGTACTTATCTAAATTAATGG 1440
 Db 1416 AATGGTTATCATTAGGCTTTGATTTATAAAACCTTGGGTACTTATCTAAATTAATGG 1475
 QY 1441 TAGTTATCTGCTTCCAGTTTGCTGATATATTTGTTGATATTAAAGTTCTTGACTTAT 1500
 Db 1476 TAGTTATCTGCTTCCAGTTTGCTGATATATTTGTTGATATTAAAGTTCTTGACTTAT 1535
 QY 1501 ATTTGGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTGAAGACATCGATATACATT 1560
 Db 1536 ATTTGGAATGGGTTCTAGTGAAGAAAGGAATGATATTTCTGAAGACATCGATATACATT 1595
 QY 1561 TATTTACACTCTGATTTCTACAATGTAGAAAATGAGAAATGCCACAATTTGATGTTG 1620
 Db 1596 TATTTACACTCTGATTTCTACAATGTAGAAAATGAGAAATGCCACAATTTGATGTTG 1655
 QY 1621 TAAAGTCACGTGAACAGAGTGTGTTGTCATCCAGGCCCTTTGCTGTTGTTTCATG 1680
 Db 1656 TAAAGTCACGTGAACAGAGTGTGTTGTCATCCAGGCCCTTTGCTGTTGTTTCATG 1715
 QY 1681 ATCTCCCTTAAGCACAATCCAACTTTAGCACAAGTTATCACACTTTGTAATTTGCAAA 1740
 Db 1716 ATCTCCCTTAAGCACAATCCAACTTTAGCACAAGTTATCACACTTTGTAATTTGCAAA 1775
 QY 1741 GAAAAGTTTCACTGTATTTGAATCAGAATGCCCTTCAACTGAAAAAACAATATCCAAAA 1800
 Db 1776 GAAAAGTTTCACTGTATTTGAATCAGAATGCCCTTCAACTGAAAAAACAATATCCAAAA 1835
 QY 1801 ATGAGGAAATGTGTTGCTCACTACGTAGAGTCCAGAGGAGACAGTCAAGTTTAAAGGTTGC 1860
 Db 1836 ATGAGGAAATGTGTTGCTCACTACGTAGAGTCCAGAGGAGACAGTCAAGTTTAAAGGTTGC 1895
 QY 1861 CTGTATCCAGTAACGTGGGGCTGTTTCCCGTGGGCTCTGAGCTGTCAAGCTTTCCCTTT 1920
 Db 1896 CTGTATCCAGTAACGTGGGGCTGTTTCCCGTGGGCTCTGAGCTGTCAAGCTTTCCCTTT 1955
 QY 1921 CTCCATGTGTTGATTTCTCTCAGGCTGGTAGCAAGTCTTGATCTTATACCAACACA 1980
 Db 1956 CTCCATGTGTTGATTTCTCTCAGGCTGGTAGCAAGTCTTGATCTTATACCAACACA 2015
 QY 1981 CAGCAACATCCAGAAATAAAGTTCT 2005
 Db 2016 CAGCAACATCCAGAAATAAAGATCT 2040

RESULT 6
 ABV25239
 ID ABV25239 standard; cDNA; 2376 BP.
 XX
 AC ABV25239;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25230.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 4947-4948; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 XX
 SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;
 Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TTGCAGGCTGCTGGGCTAGGGCTGCTGCTTCTTCCCTACAGCGGGGCACTGGGAA 60
 Db 36 TTGCAGGCTGCTGGGCTAGGGCTGCTGCTTCTTCCCTACAGCGGGGCACTGGGAA 95
 QY 61 GCGCCATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCGGCGCCGT 120
 Db 96 GCGCCATGGCACTGCAGGGCATCTCGGTGCTGAGCTGTCCGGCTGGCCCGGCGCCGT 155
 QY 121 TCTGTGCTATGCTCTGCTGACTTGGGGCGCGTGTGTGACGCGGTGACCGCGCGGCT 180
 Db 121 TCTGTGCTATGCTCTGCTGACTTGGGGCGCGTGTGTGACGCGGTGACCGCGCGGCT 180

Db 156 TCTGTGCTATGGTCCCTGGCTGACTTCGGGGCCGCTGTGTACGCTGTGACCCGGCCGCT 215
QY 181 CCCGCTAGAGAGTGAGCCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGTGACCTGAAGC 240
Db 216 CCCGCTAGACAGTGAGCCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGTGACCTGAAGC 275
QY 241 AGCCGGGGGAGCCCGCTGTGCGGGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGC 300
Db 276 AGCCGGGGGAGCCCGCTGTGCGGGCGCTGTGTGCAAGCGGTGCGATGTGCTGTGAGC 335
QY 301 CCTTCCGCGCGGTGTATGTGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAAGCGGAAA 360
Db 336 CCTCCGCGCGGTGTATGTGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAAGCGGAAA 395
QY 361 ATCCAAGGCTTATTTATGCGAGCGCTGAGTGAATTGGCCAGTCAGGAAGCTTCTGCCGCT 420
Db 396 ATCCAAGGCTTATTTATGCGAGCGCTGAGTGAATTGGCCAGTCAGGAAGCTTCTGCCGCT 455
QY 421 TAGCTGGCCACGATATCAACTATTTGGCTTGTCTCAGGTGTTCTCTCAAAAATTGGCAGAA 480
Db 456 TAGCTGGCCACGATATCAACTATTTGGCTTGTCTCAGGTGTTCTCTCAAAAATTGGCAGAA 515
QY 481 GTGTGAGAAATCCGATGCCCCGCTGAATCTCCGCTGACTTGTGCTGTGCGCTTA 540
Db 516 GTGTGAGAAATCCGATGCCCCGCTGAATCTCCGCTGACTTGTGCTGTGCGCTTA 575
QY 541 TGTGTGCACCTGGGCATTATATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGG 600
Db 576 TGTGTGCACCTGGGCATTATATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGG 635
QY 601 TCATTTGATGCAATATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTC 660
Db 636 TCATTTGATGCAATATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAATACTC 695
QY 661 AGAAATCGAGTCTGTGGGAAGCACCCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTT 720
Db 696 AGAAATCGAGTCTGTGGGAAGCACCCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTT 755
QY 721 TCTATACGACTTACAGGACAGCATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCC 780
Db 756 TCTATACGACTTACAGGACAGCATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCC 815
QY 781 AGTTCTAGAGCTGCTGATCAAAAGGACTTGAATAAAGTCTGATGAACCTCCCAATCAGA 840
Db 816 AGTTCTAGAGCTGCTGATCAAAAGGACTTGAATAAAGTCTGATGAACCTCCCAATCAGA 875
QY 841 TGAAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCACAGATGATTTGCCAAAGAAGA 900
Db 876 TGAAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCACAGATGATTTGCCAAAGAAGA 935
QY 901 CGAAGGACAGAGTGTCTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGTTCTGA 960
Db 936 CGAAGGACAGAGTGTCTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGTTCTGA 995
QY 961 CTTTGTAGGAGGTTGTTCAATCATGATCACAACAAGGAACGGGGCTCGTTATTCACCAAGTG 1020
Db 996 CTTTGTAGGAGGTTGTTCAATCATGATCACAACAAGGAACGGGGCTCGTTATTCACCAAGTG 1055
QY 1021 AGGAGCAGAGAGTGAGCCCCCGCCCTGCACCTGTGCTGTTAAACACCCAGCCATCCCTT 1080
Db 1056 AGGAGCAGAGAGTGAGCCCCCGCCCTGCACCTGTGCTGTTAAACACCCAGCCATCCCTT 1115
QY 1081 CTTTCAAAAAGGATCCTTTCATAGGAGAAACACACTGAGAGATACCTTGAAGAAATTGGAT 1140
Db 1116 CTTTCAAAAAGGATCCTTTCATAGGAGAAACACACTGAGAGATACCTTGAAGAAATTGGAT 1175
QY 1141 TCAGCCCGGGAAGATTTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGGTAA 1200
Db 1176 TCAGCCCGGGAAGATTTATCAGCTTAAGTCAAGTAAATCATTTGAAGTAAAGGTAA 1235
QY 1201 AAGCTAGTCTCTAAGTTCAGGCCCCAGGCTCAAGTGAATTGAATTAAGTCAAGT 1260
Db 1236 AAGCTAGTCTCTAAGTTCAGGCCCCAGGCTCAAGTGAATTGAATTAAGTCAAGT 1295

QY 1261 GTAGAGTAACACATTAACATTTGATGATGAGAAACATGAGGAACAGATATTAAGTGTCT 1320
Db 1296 GTAGAGTAACACATTAACATTTGATGATGAGAAACATGAGGAACAGATATTAAGTGTCT 1355
QY 1321 ACCACTTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATGATTTGAA 1380
Db 1356 ACCACTTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATGATTTGAA 1415
QY 1381 AAATGTTATCATTTAGGCTTTTGATTTTAAAACTTTGGTACTTATTAATAATTATCG 1440
Db 1416 AAATGTTATCATTTAGGCTTTTGATTTTAAAACTTTGGTACTTATTAATAATTATCG 1475
QY 1441 TAGTTATTTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTAT 1500
Db 1476 TAGTTATTTGCTTCCAGTTTGTGATATATTTGTTGATATTAAGATTTCTGACTTAT 1535
QY 1501 ATTTGAATGGCTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT 1560
Db 1536 ATTTGAATGGCTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT 1595
QY 1561 TATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAATTTGTATGTGA 1620
Db 1596 TATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAATTTGTATGTGA 1655
QY 1621 TAAAGTCAAGTGAAGACAGAGTGTATGGTTGCATCCAGGCTTTTGTCTTGGTTCATG 1680
Db 1656 TAAAGTCAAGTGAAGACAGAGTGTATGGTTGCATCCAGGCTTTTGTCTTGGTTCATG 1715
QY 1681 ATCTCCCTTAAGCACATTTCCAACTTTTAGCAACAGTTATACACACTTTGTAATTTGCAA 1740
Db 1716 ATCTCCCTTAAGCACATTTCCAACTTTTAGCAACAGTTATACACACTTTGTAATTTGCAA 1775
QY 1741 GAAAAGTTTACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAATA 1800
Db 1776 GAAAAGTTTACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAATA 1835
QY 1801 ATGAGAAATGTGTGGCTCACTACGTAGAGTCCAGAGGACAGTCAAGTTTGAAGGTGTC 1860
Db 1836 ATGAGAAATGTGTGGCTCACTACGTAGAGTCCAGAGGACAGTCAAGTTTGAAGGTGTC 1895
QY 1861 CTGTATCCAGTAAGTCTGGGCGCTGTTCCCGGTGGGTCTGTGGGCTGTCAAGCTTTCCTT 1920
Db 1896 CTGTATCCAGTAAGTCTAGGGCGCTGTTCCCGGTGGGTCTGTGGGCTGTCAAGCTTTCCTT 1955
QY 1921 CTCCATGTGTTGATTTCTCCCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACACA 1980
Db 1956 CTCCATGTGTTGATTTCTCCCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACACA 2015
QY 1981 CAGCAACATCCAGAAATAAAGTTCT 2005
Db 2016 CAGCAACATCCAGAAATAAAGATCT 2040

RESULT 7
ABV27112
ID ABV27112 standard; cDNA; 2376 BP.
XX
AC ABV27112;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27103.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX

PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 5494-5495; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
CC
XX
SQ Sequence 2376 BP; 621 A; 512 C; 609 G; 634 T; 0 other;

Query Match 99.7%; Score 1998.6; DB 23; Length 2376;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCCTTCAGCGGGCAGCTGGGAA 60
DB 36 TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCCTTCAGCGGGCAGCTGGGAA 95
QY 61 GCGCCATGGCACTGCAGGGGCATCTCGGTCTGTGAGCTGTCCGGCCTGGCCCCGGCCCGT 120
DB 96 GCGCCATGGCACTGCAGGGGCATCTCGGTCTGTGAGCTGTCCGGCCTGGCCCCGGCCCGT 155
QY 121 TCTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 156 TCTGTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 215
QY 181 CCGGCTACGACGTGAGCCCGCTTGGGGCCGGGCAAGCGCTCGCTAGTGTGCTGAGCTGAAGC 240
DB 216 CCGGCTACGACGTGAGCCCGCTTGGGGCCGGGCAAGCGCTCGCTAGTGTGCTGAGCTGAAGC 275
QY 241 AGCGCGGGGAGCGCGGCTGCTGCGGCGCTCTGTGCAAGCGGTGCGGATGTGCTGTGAGC 300
DB 276 AGCGCGGGGAGCGCGGCTGCTGCGGCGCTCTGTGCAAGCGGTGCGGATGTGCTGTGAGC 335
QY 301 CCTCCGCGCGGCTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAA 360
DB 336 CCTCCGCGCGGCTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAA 395
QY 361 ATCCAAGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGCT 420
DB 396 ATCCAAGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGCT 455
QY 421 TAGCTGGCCACGATATCAACTATTGGCTTGTGCAAGTGTCTCTCAAAAATGGCAGAA 480
|||||

DB 456 TAGTGGCCACGATATCAACTATTGGCTTGTGCAAGTGTCTCTCAAAAATGGCAGAA 515
QY 481 GTGTGAGAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGTGGCTTA 540
DB 516 GTGTGAGAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGTGGCTTA 575
QY 541 TGTGTGCACTGGGCATTATATGCTCTTTTGTGACCGGCACAGCCTGGCAAGGGTCAAG 600
DB 576 TGTGTGCACTGGGCATTATATGCTCTTTTGTGACCGGCACAGCCTGGCAAGGGTCAAG 635
QY 601 TCATTGATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGGAAGAACTC 660
DB 636 TCATTGATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGGAAGAACTC 695
QY 661 AGAAATCGAGTCTGTGGAAGCACTTCGAGACAGAGAAGAGTGTGATGGTGAGACACTT 720
DB 696 AGAAATCGAGTCTGTGGAAGCACTTCGAGACAGAGAAGAGTGTGATGGTGAGACACTT 755
QY 721 TCTATACGACTTACAGACAGACAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCC 780
DB 756 TCTATACGACTTACAGACAGACAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCC 815
QY 781 AGTTTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 840
DB 816 AGTTTACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGA 875
QY 841 TGAGCATGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTGTGCAAGAAGA 900
DB 876 TGAGCATGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTGTGCAAGAAGA 935
QY 901 CGAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGA 960
DB 936 CGAAGCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGA 995
QY 961 CTTTGGAGGAGTGTTCATCATGATCAACAAGAAGAGGGCTCGTTTATCACCAGTG 1020
DB 996 CTTTGGAGGAGTGTTCATCATGATCAACAAGAAGAGGGCTCGTTTATCACCAGTG 1055
QY 1021 AGGACGAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 1080
DB 1056 AGGACGAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTT 1115
QY 1081 CTTTCAAAAGGATCTTTTCATATGAGAGAACAACACTGAGAGATACTTGAAGAATTGGAT 1140
DB 1116 CTTTCAAAAGGATCTTTTCATATGAGAGAACAACACTGAGAGATACTTGAAGAATTGGAT 1175
QY 1141 TCAGCCGGAAGAGATTATACCTTAACCTCAGATAAAATCATGAAAGTAATAGGTAA 1200
DB 1176 TCAGCCGGAAGAGATTATACCTTAACCTCAGATAAAATCATGAAAGTAATAGGTAA 1235
QY 1201 AAGCTAGTCTCTAATCTCCAGGCCACGCGCTCAAGTGAATTGAATTAATTAAGTAA 1260
DB 1236 AAGCTAGTCTCTAATCTCCAGGCCACGCGCTCAAGTGAATTGAATTAATTAAGTAA 1295
QY 1261 GTAGAGTAACACATTAACATTGTATGATGGAACAACATGAGAGAACAGTATTACAGTTCCT 1320
DB 1296 GTAGAGTAACACATTAACATTGTATGATGGAACAACATGAGAGAACAGTATTACAGTTCCT 1355
QY 1321 ACCACTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATGAATTCCTAA 1380
DB 1356 ACCACTTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGATGATGAATTCCTAA 1415
QY 1381 AAATGTTATCATTAGGGCTTTGATTTATAAACTTTGGTACTTATTAATAATTAATG 1440
DB 1416 AAATGTTATCATTAGGGCTTTGATTTATAAACTTTGGTACTTATTAATAATTAATG 1475
QY 1441 TAGTTATTTCTGCCCTTCCAGTTGCTTGATATATTGTTGATATTGAATTTCTGACTTAT 1500
DB 1476 TAGTTATTTCTGCCCTTCCAGTTGCTTGATATATTGTTGATATTGAATTTCTGACTTAT 1535
QY 1501 ATTTGAATGGGTTCTAGTGAAGAAAGGAATGATATATTTCTGAAGACATCGATATACATT 1560
DB 1536 ATTTGAATGGGTTCTAGTGAAGAAAGGAATGATATATTTCTGAAGACATCGATATACATT 1595
|||||

QY 1561 TATTACTCTGTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGTATGGTGA 1620
|||||
Db 1596 TATTACTCTGTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGTATGGTGA 1655
QY 1621 TAAAAGTCACGTGAACACAGATGATGGTTCATCCAGCCCTTTGTCTGGTTCATG 1680
|||||
Db 1656 TAAAAGTCACGTGAACACAGATGATGGTTCATCCAGCCCTTTGTCTGGTTCATG 1715
QY 1681 ATCTCCCTCTAAGCACATTCCTCAACCTTTAGCAACAGTTATCACACTTTGTAATTTGCAA 1740
|||||
Db 1716 ATCTCCCTCTAAGCACATTCCTCAACCTTTAGCAACAGTTATCACACTTTGTAATTTGCAA 1775
QY 1741 GAAAAGTTTCACCTGTAATGAATCAGAAATGCCCTTCACTGAAAAAACAATATCCAAATA 1800
|||||
Db 1776 GAAAAGTTTCACCTGTAATGAATCAGAAATGCCCTTCACTGAAAAAACAATATCCAAATA 1835
QY 1801 ATGAGGAAATGTGTGGCTCAGTACGTAAGAGTCCAGAGGACAGTCACTTTTAGGGTTC 1860
|||||
Db 1836 ATGAGGAAATGTGTGGCTCAGTACGTAAGAGTCCAGAGGACAGTCACTTTTAGGGTTC 1895
QY 1861 CTGTATCCAGTAACTCGGGGCTGTTCCTCCGCTGGGCTCTGGGCTGTACGCTTCCCTT 1920
|||||
Db 1896 CTGTATCCAGTAACTCGGGGCTGTTCCTCCGCTGGGCTCTGGGCTGTACGCTTCCCTT 1955
QY 1921 CTCCATGTGTGATTTCTCCTCAGGCTGCTAGCAAGTCTGATCTTATACCCCAACACA 1980
|||||
Db 1956 CTCCATGTGTGATTTCTCCTCAGGCTGCTAGCAAGTCTGATCTTATACCCCAACACA 2015
QY 1981 CAGCAACATCCAGAAATTAAGTCT 2005
|||||
Db 2016 CAGCAACATCCAGAAATTAAGTCT 2040

RESULT 8
ABK92152
ID ABK92152 standard; DNA; 2068 BP.
AC ABK92152;
XX 15-AUG-2002 (first entry)
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #38.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afari D, Hevezi P;
XX
DR WPI: 2002-471335/50.
DR P-PSDB; ABG61837.
XX

PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue
XX
PS Claim 22; Page 329; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.
XX
SQ Sequence 2068 BP; 555 A; 436 C; 528 G; 548 T; 1 other;
Query Match 97.3%; Score 1950.8; DB 24; Length 2068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1985; Conservative 0; Mismatches 18; Indels 4; Gaps 2;
QY 1 TTGACAGCTGCTGGGCTGGGCTAAGGGCTGCTACGTTCTCTACAGGGGGCAGCTGGAA 60
Db 24 TTGACAGCTGCTGGGCTGGGCTAAGGGCTGCTACGTTCTCTACAGGGGGCAGCTGGAA 83
QY 61 GCGCCATGCGACATGACGGCATCTCGTGTGAGAGCTGTCCGGCCCGCCCGCCGCT 120
Db 84 GCGCCATGCGACATGACGGCATCTCGTGTGAGAGCTGTCCGGCCCGCCCGCCGCTN 143
QY 121 TCTGTGCTATGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 144 TCTGTGCTATGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY 181 CCCGCTACGAGCTGAGCGGCTTGGCGGGGCAAGCGCTGCTAGTCTGACCTGAAGC 240
Db 204 CCCGCTACGAGCTGAGCGGCTTGGCGGGGCAAGCGCTGCTAGTCTGACCTGAAGC 263
QY 241 AGCCGGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 300
Db 264 AGCCGGGGG--AGCCGGCTGTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGC 321
QY 301 CCTTCGCGCGGCTGTGTGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAA 360
Db 322 CCTTCGCGCGGCTGTGTGAGAGAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAA 381
QY 361 ATCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGT--CAGGAAGCTTTCGCCG 418
Db 382 ATCCAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGT--CAGGAAGCTTTCGCCG 441
QY 419 GTTAGCTGGCCACGATATCACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAG 478
Db 442 GTTAGCTGGCCACGATATCACTATTGGCTTTGTCAAGGTGTTCTCAAAAATTGGCAG 501
QY 479 AAGTGTGAGAAATCCGATATGCCCGCGTGAATCTCCTGGCTGACTTTGGTGGTGGCCT 538
Db 502 AAGTGTGAGAAATCCGATATGCCCGCGTGAATCTCCTGGCTGACTTTGGTGGTGGCCT 561
QY 539 TATGTGTCACTGGGCAATATATAGGCTTTTGAACCCACACGCACTGGCAAGGCTCA 598
Db 562 TATGTGTCACTGGGCAATATATAGGCTTTTGAACCCACACGCACTGGCAAGGCTCA 621
QY 599 GGTCAATGATGCAAAATATGTTGGAAGCAACAGCATATTTAAGTCTTTTCTGTGGAAC 658
|||||

Db 622 GGTGATGATGCAAAATATGGTGGAGGAACAGCAATTTAAGTCTTTCTGTGGAAAAAC 681
QY 659 TCAGAAATCGAGTCTGTGGGAAGCACCTCGAGACAGAACATGTTGGATGGTGAGCACC 718
Db 682 TCAGAAATCGAGTCTGTGGGAAGCACCTCGAGACAGAACATGTTGGATGGTGAGCACC 741
QY 719 TTTCTATACGACTTACAGGACAGCAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACC 778
Db 742 TTTCTATACGACTTACAGGACAGCAGATGGGGAATTCATGCGCTGTGGAGCAATAGAACC 801
QY 779 CCAGTTCTACGAGCTGCTGATCAAAAGACCTTGACCTAAAGTCTGATGAACCTCCCAATCA 838
Db 802 CCAGTTCTACGAGCTGCTGATCAAAAGACCTTGACCTAAAGTCTGATGAACCTCCCAATCA 861
QY 839 GATGAGCATGATGATGTTGCCAGAAATGAAGAAAGTTTGCAGATGTATTCGAAAGAA 898
Db 862 GATGAGCAGCAGATGATTTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTCGAAAGAA 921
QY 899 GACGAAGCAGAGTGGTGTCAAAATCTTTGACGGCAGACAGATGCCCTGTGTACTCCGGTCT 958
Db 922 GACGAAGCAGAGTGGTGTCAAAATCTTTGACGGCAGACAGATGCCCTGTGTACTCCGGTCT 981
QY 959 GACTTTGAGGAGGTGTTTCATCATGATCACAACAGGAACGGGGCTCGTTATTCACCAG 1018
Db 982 GACTTTGAGGAGGTGTTTCATCATGATCACAACAGGAACGGGGCTCGTTATTCACCAG 1041
QY 1019 TGAGGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCC 1078
Db 1042 TGAGGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCC 1101
QY 1079 TTCTTTCAAAAGGATCCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTTGG 1138
Db 1102 TTCTTTCAAAAGGATCCCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTTGG 1161
QY 1139 ATTCAAGCCGGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATAAGT 1198
Db 1162 ATTCAAGCCGGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAGTAATAAGT 1221
QY 1199 AAAAGCTAGTCTCTAATCTTCCAGGGCCACGGCTCAAGTGAATTTGAATACTGCAATTTACA 1258
Db 1222 AAAAGCTAGTCTCTAATCTTCCAGGGCCACGGCTCAAGTGAATTTGAATACTGCAATTTACA 1281
QY 1259 GTGTAGAGTAACACATAACATTGTATGCATGGAACATGGAGGAACAGTATTAACAGTGTCTC 1318
Db 1282 GTGTAGAGTAACACATAACATTGTATGCATGGAACATGGAGGAACAGTATTAACAGTGTCTC 1341
QY 1319 CTACCACCTCTAATCAAGAAAGAAATTACAGACTCTGATCTACAGTGATGATGAATTCT 1378
Db 1342 CTACCACCTCTAATCAAGAAAGAAATTACAGACTCTGATCTACAGTGATGATGAATTCT 1401
QY 1379 AAAAATGGTTATCATAGGGCTTTTGATTTATATAAACTTTGGGTACTTATTAATAATTAT 1438
Db 1402 AAAAATGGTTATCATAGGGCTTTTGATTTATATAAACTTTGGGTACTTATTAATAATTAT 1461
QY 1439 GGTAGTTATTTCCCTCCAGTTTGTGATTAATTTGTTGATATTAAGATCTTGACTT 1498
Db 1462 GGTAGTTATTTCCCTCCAGTTTGTGATTAATTTGTTGATATTAAGATCTTGACTT 1521
QY 1499 ATATTTGAATGGTCTTAGTGAAGAAAGAAATATATATCTTGAAGACATCATATACA 1558
Db 1522 ATATTTGAATGGTCTTAGTGAAGAAAGAAATATATATCTTGAAGACATCATATACA 1581
QY 1559 TTTATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGGAATGCCACAAATTTGATGCT 1618
Db 1582 TTTATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGGAATGCCACAAATTTGATGCT 1641
QY 1619 GATAAAAGTCACGTGAACAGAGTGAATGGTTGTCATCCAGGCCCTTTGTCTGTGGTGTCA 1678
Db 1642 GATAAAAGTCACGTGAACAGAGTGAATGGTTGTCATCCAGGCCCTTTGTCTGTGGTGTCA 1701
QY 1679 TGATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGTTATCACACCTTTGTAATTTGCA 1738
Db 1702 TGATCTCCCTCTAAGCACATTTCCAAACTTTAGCAACAGTTATCACACCTTTGTAATTTGCA 1761

QY 1739 AAGAAAAGTTTACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAA 1798
Db 1762 AAGAAAAGTTTACCTGTATTTGAATCAGAAATGCCCTTCAACTGAAAAAACATATCCAAA 1821
QY 1799 TAATGAGGAATGTGTGGCTCCTACTACGTAGAGTCCAGAGGACAGTCACTTTAGGGTT 1858
Db 1822 TAATGAGGAATGTGTGGCTCCTACTACGTAGAGTCCAGAGGACAGTCACTTTAGGGTT 1881
QY 1859 GCCTGTATCCAGTAACTCGGGGGCTGTTCCCGTGGGTCTCTGGGCTGTACAGCTTTCCT 1918
Db 1882 GCCTGTATCCAGTAACTCGGGGGCTGTTCCCGTGGGTCTCTGGGCTGTACAGCTTTCCT 1941
QY 1919 TTCTCCATGTGTTGATTTCTCCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACA 1978
Db 1942 TTCTCCATGTGTTGATTTCTCCTCAGGCTGGTAGCAAGTTCTGATCTTATACCAACA 2001
QY 1979 CACAGCAACATCCAGAAATAAAGTTCT 2005
Db 2002 CACAGCAACATCCAGAAATAAAGATCT 2028

RESULT 9
AAD38606
ID AAD38606 standard; cdna; 3023 BP.
XX AC AAD38606;
XX AC AAD38606;
XX DT 23-SEP-2002 (first entry)
XX DE Human alpha-methylacyl-CoA racemase splice variant, SV3 cdna.
XX KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
XX KW cytosolic; SV3; gene; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS Location/Qualifiers
FT 90..686
FT /*tag= a
FT /product= "Human SV3 protein"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US30532.
XX PR 28-SEP-2000; 2000US-236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX PI Richardson J, Monahan J;
XX
XX DR WPI; 2002-405070/43.
XX DR P-PSDB; AAE23974.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase -
XX
PS Claim 54; Fig 7; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether
CC an individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of
CC alpha-methylacyl-CoA racemase. Sequences of the invention are useful
CC in diagnostic methods, drug screening assays, and in treating or
CC preventing cancer, e.g. prostate cancer. The present sequence is human
CC alpha-methyl-acyl-CoA racemase splice variant, SV3 cdna.
XX

SQ	Sequence 3023 BP; 846 A; 621 C; 710 G; 846 T; 0 other;
Query Match	83.4%; Score 1671.4; DB 24; Length 3023;
Best Local Similarity	91.9%; Pred. No. 0;
Matches 1843; Conservative	0; Mismatches 1; Indels 161; Gaps 1;
QY	1 TTGCAGGCTGCTGGGCTGGGGCTAAGGCTCTCAGTTTCCTTCAGCGGGCACTGGGAA 60
DB	25 TTGCAGGCTGCTGGGCTGGGGCTAAGGCTCTCAGTTTCCTTCAGCGGGCACTGGGAA 84
QY	61 GCGCCATGGCACTGCAGGCACTCTCGGTCTGAGACTGTCCGGCTGGCCCGGGCCGCT 120
DB	85 GCGCCATGGCACTGCAGGCACTCTCGGTCTGAGACTGTCCGGCTGGCCCGGGCCGCT 144
QY	121 TCTGTGCTATGCTCCTGGCTGACTTCGGGGCGCTGTGTGACCGGTGACCGCGCGCT 180
DB	145 TCTGTGCTATGCTCCTGGCTGACTTCGGGGCGCTGTGTGACCGGTGACCGCGCGCT 204
QY	181 CCCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 240
DB	205 CCCGCTACGAGCTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGC 264
QY	241 AGCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGCTGAGC 300
DB	265 AGCCGGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGCTGAGC 324
QY	301 CCTTCCGCGCGGCTGTCATGAGAAACTCCAGCTGGGCCCAAGATTCGACGGGGAAA 360
DB	325 CCTTCCGCGCGGCTGTCATGAGAAACTCCAGCTGGGCCCAAGATTCGACGGGGAAA 384
QY	361 ATCCAAGGCTTATTTATGCCAGGCTGAGTTGGCCAGTCAGGAAGCTTCTGCCGCT 420
DB	385 ATCCAAGGCTTATTTATGCCAGGCTGAGTTGGCCAGTCAGGAAGCTTCTGCCGCT 444
QY	421 TAGCTGGCCAGCATATCAACTATTGGCTTGTCAAGGTCTCTCAAAAAATTGGCAGAA 480
DB	445 TAGCTGGCCAGCATATCAACTATTGGCTTGTCA----- 479
QY	481 GTGTGAGAAATCCGTATGCCCGCTGAATCTCTGCTGACTTGTGTGGCTTGA 540
DB	480 ----- 479
QY	541 TGTGTGACTGGGCAATTATAATGCGCTTTTGAACCGCACACGCACTGGCAAGGCTCAGG 600
DB	480 ----- 479
QY	601 TCATTGATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTCTGTGAAAACTC 660
DB	480 -----GGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGAAAACTC 523
QY	661 AGAAATCGAGTCTGTGGGAACCACTCGAGGACAGAACATGTGGATGTGGAGCACCTT 720
DB	524 AGAAATCGAGTCTGTGGGAACCACTCGAGGACAGAACATGTGGATGTGGAGCACCTT 583
QY	721 TCTATACGACTTACAGGACAGACAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCC 780
DB	584 TCTATACGACTTACAGGACAGACAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCC 643
QY	781 AGTTCTACGAGCTGCTGATCAAAAGGACTTGAAGTCAAGTCTGATGAAGTTCCCAATCAGA 840
DB	644 AGTTCTACGAGCTGCTGATCAAAAGGACTTGAAGTCTGATGAAGTTCCCAATCAGA 703
QY	841 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAAAGAGA 900
DB	704 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAAAGAGA 763
QY	901 CGAAGGCGAGTGGTGTCAAAATCTTTGACGGGACAGATGCTGTGACTCGGGTTCTGA 960
DB	764 CGAAGGCGAGTGGTGTCAAAATCTTTGACGGGACAGATGCTGTGACTCGGGTTCTGA 823
QY	961 CTTTGTAGAGGTTGTTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAAGTG 1020
DB	824 CTTTGTAGAGGTTGTTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAAGTG 883

QY	1021 AGGAGCAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCCAGCCATCCCTT 1080
DB	884 AGGAGCAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCCAGCCATCCCTT 943
QY	1081 CTTTCAAAAGCGATCCTTTCATAGGAGAACACACTGAGAGATTAAGTAATTTGGAT 1140
DB	944 CTTTCAAAAGCGATCCTTTCATAGGAGAACACACTGAGAGATTAAGTAATTTGGAT 1003
QY	1141 TCAGCCCGGCAAGAGATTTATCAGCTTAAGTCAAGTAAATATCATTTGAAGTTAA 1200
DB	1004 TCAGCCCGGCAAGAGATTTATCAGCTTAAGTCAAGTAAATATCATTTGAAGTTAA 1063
QY	1201 AAGCTAGTCTTAAGTTCAGGCCCCACGGCTCAAGTGAATTTGAATACATTTACAGT 1260
DB	1064 AAGCTAGTCTTAAGTTCAGGCCCCACGGCTCAAGTGAATTTGAATACATTTACAGT 1123
QY	1261 GTAGAGTAACACATTAACATTTGTATGATGGAAGAACATGAGGAACAGTATTACAGTCTCT 1320
DB	1124 GTAGAGTAACACATTAACATTTGTATGATGGAAGAACATGAGGAACAGTATTACAGTCTCT 1183
QY	1321 ACCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGAATCTTAA 1380
DB	1184 ACCACTCTAATCAAGAAAGAAATTTACAGACTCTGATTTCTACAGTATGATTTGAATCTTAA 1243
QY	1381 AAATGTTATCATTTAGGCTTTTGAATTTAAACTTTGGCTACTTATTAATAATTATG 1440
DB	1244 AAATGTTATCATTTAGGCTTTTGAATTTAAACTTTGGCTACTTATTAATAATTATG 1303
QY	1441 TAGTTATTTCTGCTTCCAGTTTGTGATATATTGTTGATATTAAAGATTCTTGACTTAT 1500
DB	1304 TAGTTATTTCTGCTTCCAGTTTGTGATATATTGTTGATATTAAAGATTCTTGACTTAT 1363
QY	1501 ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT 1560
DB	1364 ATTTGAATGGGTTCTAGTGAAGAAAGAAATGATATATTTCTGAAGACATCGATATACAT 1423
QY	1561 TATTTACACTCTTGATTTCAATGTAGAAATGAGAAATGCCACAATTTGTATGTGA 1620
DB	1424 TATTTACACTCTTGATTTCAATGTAGAAATGAGAAATGCCACAATTTGTATGTGA 1483
QY	1621 TAAAGTCAAGTGAAGACAGATGATTTGGTTGCATCCAGGCTTTTGTCTGTGGTTCATG 1680
DB	1484 TAAAGTCAAGTGAAGACAGATGATTTGGTTGCATCCAGGCTTTTGTCTGTGGTTCATG 1543
QY	1681 ATCTCCCTCAAGCACATTCCAAACCTTTAGCAACAGTTTACACACTTTGTAATTGGCAAA 1740
DB	1544 ATCTCCCTCAAGCACATTCCAAACCTTTAGCAACAGTTTACACACTTTGTAATTGGCAAA 1603
QY	1741 GAAAAGTTTCAACTGTATTTGAATCAGAAATGCTTCAACTGAAAAAAACAATATCCAAATA 1800
DB	1604 GAAAAGTTTCAACTGTATTTGAATCAGAAATGCTTCAACTGAAAAAAACAATATCCAAATA 1663
QY	1801 ATGAGGAATGTGTTGGCTCACTACGTAGAGTCCAGAGGACAGTCAAGTTTAAAGGTTGC 1860
DB	1664 ATGAGGAATGTGTTGGCTCACTACGTAGAGTCCAGAGGACAGTCAAGTTTAAAGGTTGC 1723
QY	1861 CTGTATCCAGTAAGTCAAGGCTGTTCCTGAGGCTGTGGGCTGTGAGCTTTCCTT 1920
DB	1724 CTGTATCCAGTAAGTCAAGGCTGTTCCTGAGGCTGTGGGCTGTGAGCTTTCCTT 1783
QY	1921 CTCATGTGTTGATTTCTCCTCAGGCTGTAGCAAGTTCTGATCTTAATACCAACACA 1980
DB	1784 CTCATGTGTTGATTTCTCCTCAGGCTGTAGCAAGTTCTGATCTTAATACCAACACA 1843
QY	1981 CAGCAACATCCAGAATAAAGTTCT 2005
DB	1844 CAGCAACATCCAGAATAAAGATCT 1868

RESULT 10
AAH13696
ID AAH13696 standard; cDNA; 1674 BP.

XX AAH13696;
AC
XX 26-JUN-2001 (first entry)
DT
XX Human cDNA sequence SEQ ID NO:10567.
DE
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
KM
XX Homo sapiens.
OS
XX EP1074617-A2.
PN
XX 07-FEB-2001.
PD
XX
XX 28-JUL-2000; 2000EP-0116126.
PE
XX
XX 29-JUL-1999; 99JP-0248036.
PR
XX 27-AUG-1999; 99JP-0300253.
PR
XX 11-JAN-2000; 2000JP-0118776.
PR
XX 02-MAY-2000; 2000JP-0183767.
PR
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX WPI; 2001-318749/34.
DR
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX Claim 8; SEQ ID 10567; 2537pp + CD ROM; English.
PS
XX
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1674 BP; 432 A; 349 C; 451 G; 442 T; 0 other;

Query Match 82.5%; Score 1653.2; DB 22; Length 1674;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1655; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGCAGGCTGTGGGCTGAAGGCTGCTCAGTTCTTCTTACGCGGACACTGGGAA 60
DB 17 TTGCAGGCTGTGGGCTGAAGGCTGCTCAGTTCTTCTTACGCGGACACTGGGAA 76
QY 61 GCGGCATGGCACTGCAGGCACTCTGGTCTGTGAGCTGTCCGGCCTGGCCCCGGCCGT 120
DB 77 GCGGCATGGCACTGCAGGCACTCTGGTCTGTGAGCTGTCCGGCCTGGCCCCGGCCGT 136

QY 121 TCTGTGCTATGCTCTGGCTGACTTTCGGGGCGCGTGTGCTACGCGGTGAGCCGCGCGCT 180
DB 137 TCTGTGCTATGCTCTGGCTGACTTTCGGGGCGCGTGTGCTACGCGGTGAGCCGCGCGCT 196
QY 181 CCCGCTACGACGTGAGCCGCTTGGCCGGGGGCAAGCGCTGCTAGTGTGACCTGGAAGC 240
DB 197 CCCGCTACGACGTGAGCCGCTTGGCCGGGGGCAAGCGCTGCTAGTGTGACCTGGAAGC 256
QY 241 AGCCGCGGGGAGCCCGCGCTGCTGCGCGCTGTGCAAGCGGTCGATGTGCTGAGAGC 300
DB 257 AGCCGCGGGGAGCCCGCGCTGCTGCGCGCTGTGCAAGCGGTCGATGTGCTGAGAGC 316
QY 301 CCTTCCGCGCGCGGTGTCTATGAGAAACTCCAGCTGGGCCCCAGAGATTCTGACGCGGAAA 360
DB 317 CCTTCCGCGCGCGGTGTCTATGAGAAACTCCAGCTGGGCCCCAGAGATTCTGACGCGGAAA 376
QY 361 ATCCAAGCCTTATTATGCGCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCGGT 420
DB 377 ATCCAAGCCTTATTATGCGCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCGGT 436
QY 421 TAGCTGGCCACGATATCAACTATTTGGCTTTGTACAGGTCTCTCAAAAATGCGAGAA 480
DB 437 TAGCTGGCCACGATATCAACTATTTGGCTTTGTACAGGTCTCTCAAAAATGCGAGAA 496
QY 481 GTGGTGAAGATCCGTATGCCCGCGCTGAATCTCGTGGCTGACTTGTGCTGCTGCTGCTTA 540
DB 497 GTGGTGAAGATCCGTATGCCCGCGCTGAATCTCGTGGCTGACTTGTGCTGCTGCTGCTTA 556
QY 541 TGTGTGCACTGGGCACTTATATGCGCTCTTTTGACCGCAGCAGCACTGGCAAGGTCAGG 600
DB 557 TGTGTGCACTGGGCACTTATATGCGCTCTTTTGACCGCAGCAGCACTGGCAAGGTCAGG 616
QY 601 TCATTGATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTC 660
DB 617 TCATTGATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTC 676
QY 661 AGAAATCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGGATGTTGGAGCACTT 720
DB 677 AGAAATCGAGTCTGTGGGAAGCACTCGAGGACAGACATGTTGGATGTTGGAGCACTT 736
QY 721 TCTATACGACTTACAGGACAGACAGATGGGAATTTCATGCGCTGTTGAGCAATAGAACCC 780
DB 737 TCTATACGACTTACAGGACAGACAGATGGGAATTTCATGCGCTGTTGAGCAATAGAACCC 796
QY 781 AGTTCTACGAGCTGTGATCAAAAGCACTTGCACTAAAGTCTGATGAACCTTCCCAATCAGA 840
DB 797 AGTTCTACGAGCTGTGATCAAAAGCACTTGCACTAAAGTCTGATGAACCTTCCCAATCAGA 856
QY 841 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCAGATGATTTTGGCAAGAAGA 900
DB 857 TGAGCATGATGATTTGGCCAGAAATGAAGAAGATTTCAGATGATTTTGGCAAGAAGA 916
QY 901 CGAAGCCAGAGTGTGTCAAAATCTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGA 960
DB 917 CGAAGCCAGAGTGTGTCAAAATCTTTGACGGCAGACAGATGCCGTGTGACTCCGGTCTGA 976
QY 961 CTTTGTAGGAGGTGTTTCATCATGATCACAACAAGGAAGCGGGCTGTTTATCACCAGTG 1020
DB 977 CTTTGTAGGAGGTGTTTCATCATGATCACAACAAGGAAGCGGGCTGTTTATCACCAGTG 1036
QY 1021 AGGACGAGAGCTGAGCCCGCGCTGACCTCTGCTTTAAACACCCAGCCATCCCTT 1080
DB 1037 AGGACGAGAGCTGAGCCCGCGCTGACCTCTGCTTTAAACACCCAGCCATCCCTT 1096
QY 1081 CTTTCAAAAGGATCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTGGAT 1140
DB 1097 CTTTCAAAAGGATCTTTCATAGGAGAACACACTGAGAGATACTTGAAGAAATTGGAT 1156
QY 1141 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATTAATAATCATTTGAAAGTAATAGGTA 1200
DB 1157 TCAGCCGCGAAGAGATTATCAGCTTAACCTCAGATTAATAATCATTTGAAAGTAATAGGTA 1216

QY 1201 AAGTAGTCTCTACTTCCAGGCCACGGCTCAAGTGAATTGTAATCTGATTTACAGT 1260
|||||
Db 1217 AAGTAGTCTCTACTTCCAGGCCACGGCTCAAGTGAATTGTAATCTGATTTACAGT 1276
|||||
QY 1261 GTAGAGTAACATTAACATTTGATGATGAGAAACATGAGAAACAGTATTTACAGTGTCT 1320
|||||
Db 1277 GTAGAGTAACATTAACATTTGATGATGAGAAACATGAGAAACAGTATTTACAGTGTCT 1336
|||||
QY 1321 ACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA 1380
|||||
Db 1337 ACCACTCTAATCAAGAAAGAAATTACAGACTCTGATTTCTACAGTGAATTTGAATTTCTAA 1396
|||||
QY 1381 AAATGTTATCATTTAGGCTTTTGTATTTATAAACTTTGGTACTTATATAATTTATGG 1440
|||||
Db 1397 AAATGTTATCATTTAGGCTTTTGTATTTATAAACTTTGGTACTTATATAATTTATGG 1456
|||||
QY 1441 TAGTTATTTGCTCTTCCAGTTTCTGATATATTGTTGATATTAAAGATTCTTGACTTAT 1500
|||||
Db 1457 TAGTTATTTGCTCTTCCAGTTTCTGATATATTGTTGATATTAAAGATTCTTGACTTAT 1516
|||||
QY 1501 ATTTGAATGGGCTTCTAGTGAAGAAAGATGATATATTCTTGAAGACATCATATACATT 1560
|||||
Db 1517 ATTTGAATGGGCTTCTAGTGAAGAAAGATGATATATTCTTGAAGACATCATATACATT 1576
|||||
QY 1561 TATTTACACTCTTGATTTCTACAATGTAGAAATAGAGAAATGCCACAATTTGTATGCTGA 1620
|||||
Db 1577 TATTTACACTCTTGATTTCTACAATGTAGAAATAGAGAAATGCCACAATTTGTATGCTGA 1636
|||||
QY 1621 TAAAGTCAAGTGAAGACAGTGTGTTGTCATCCAG 1658
|||||
Db 1637 TAAAGTCAAGTGAAGACAGTGTGTTGTCATCCAG 1674
|||||

RESULT 11
AAV61199
ID AAV61199 standard; cDNA; 1621 BP.
XX
AC AAV61199;
XX
DT 06-JAN-1999 (first entry)
XX
DE Full length cDNA sequence of prostate tumour clone F1-12.
XX
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN W09837093-A2.
XX
PD 27-AUG-1998.
XX
PE 25-FEB-1998; 98WO-US03492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI: 1998-609886/51.
DR P-PSDB: AAW71867.
XX
XX Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 76-77; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by

CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other:
Query Match 78.5%; Score 1574.2; DB 19; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1576; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CGCCATGGCACTGCAGGCGATCTCGGTGAGAGCTTCGGCCCTGGCCCGGCGCTT 121
|||||
Db 1 CGCCATGGCACTGCAGGCGATCTCGGTGAGAGCTTCGGCCCTGGCCCGGCGCTT 60
|||||
QY 122 CTGTGCTATGCTCTGCTGACTTCGGGCGCGCTGTGTACGCGTGAACCGCGGCTC 181
|||||
Db 61 CTGTGCTATGCTCTGCTGACTTCGGGCGCGCTGTGTACGCGTGAACCGCGGCTC 120
|||||
QY 182 CCGCTACGACGTGAGCCGCTTGCGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 241
|||||
Db 121 CCGCTACGACGTGAGCCGCTTGCGCGGCGCAAGCGCTCGCTAGTGTGACCTGAAGCA 180
|||||
QY 242 GCCGCGGAGAGCCGCGTGTGCTGCGGCGCTGTGCAAGCGGTGATGCTGTGAGCC 301
|||||
Db 181 GCCGCGGAGAGCCGCGTGTGCTGCGGCGCTGTGCAAGCGGTGATGCTGTGAGCC 240
|||||
QY 302 CTTCGCGCGCGGTGTGATGAGAAATCTCAAGCTGGCGCCAGAGATTCTGACGGGAAAA 361
|||||
Db 241 CTTCGCGCGCGGTGTGATGAGAAATCTCAAGCTGGCGCCAGAGATTCTGACGGGAAAA 300
|||||
QY 362 TCCAAGGCTTATTATGCCAAGGCTGAGTGGATTGGCCAGTCAGAGACTTCTGCCGTT 421
|||||
Db 301 TCCAAGGCTTATTATGCCAAGGCTGAGTGGATTGGCCAGTCAGAGACTTCTGCCGTT 360
|||||
QY 422 AGCTGGCAGCATATCACTATTGCTTGTGACGCTCTCTCAAAATTGGCAGAG 481
|||||
Db 361 AGCTGGCAGCATATCACTATTGCTTGTGACGCTCTCTCAAAATTGGCAGAG 420
|||||
QY 482 TGGTGAAGATCCGTATGCCCCGCTGAATCTCTGCGTGAATTTGCTGTGCTGCTTAT 541
|||||
Db 421 TGGTGAAGATCCGTATGCCCCGCTGAATCTCTGCGTGAATTTGCTGTGCTGCTTAT 480
|||||
QY 542 GTGTGACATGGGCGATTAATATGCGCTTTTGGACCGCACAGCAGCTGGCAAGGTCAGT 601
|||||
Db 481 GTGTGACATGGGCGATTAATATGCGCTTTTGGACCGCACAGCAGCTGGCAAGGTCAGT 540
|||||
QY 602 CATTGATCAAAATATGTTGGAAGGAAGACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 661
|||||
Db 541 CATTGATCAAAATATGTTGGAAGGAAGACAGCATATTTAAGTCTTTTCTGTGAAAACTCA 600
|||||
QY 662 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGTTGGAGCACCTTT 721
|||||
Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGATGTTGGAGCACCTTT 660
|||||
QY 722 CTATACGACTTACAGACAGCAGATGGGGAATTCAATGCTGTGAGCAATAGAACCCCA 781
|||||
Db 661 CTATACGACTTACAGACAGCAGATGGGGAATTCAATGCTGTGAGCAATAGAACCCCA 720
|||||
QY 782 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGAT 841
|||||
Db 721 GTTCTACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGAT 780
|||||
QY 842 GAGCATGATGATTTGGCCGAATGAAGAAGAAGTTCAGATGTATTGCAAGAAGAGAC 901
|||||
Db 781 GAGCATGATGATTTGGCCGAATGAAGAAGAAGTTCAGATGTATTGCAAGAAGAGAC 840
|||||
QY 902 GAAGGACAGTGTGTCAAACTTTGACGCGCACAGATGCTGTGACTCCGGTCTGAC 961
|||||
Db 841 GAAGGACAGTGTGTCAAACTTTGACGCGCACAGATGCTGTGACTCCGGTCTGAC 900
|||||
QY 962 TTTTGAAGAGTGTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA 1021
|||||
Db 901 TTTTGAAGAGTGTGTTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA 960
|||||

QY	722	CTATACGACTTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	781
Db	661	CTATACGACTTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCA	720
QY	782	GTTCCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTGCCAATCAGAT	841
Db	721	GTTCCTACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTGCCAATCAGAT	780
QY	842	GAGCATGGATGATTGGCCAGAAATGAAGAAGATTGGACATGTATTTGCCAAAGAAGAC	901
Db	781	GAGCATGGATGATTGGCCAGAAATGAAGAAGATTGGACATGTATTTGCCAAAGAAGAC	840
QY	902	GAAGCGACAGATGCGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTGAC	961
Db	841	GAAGCGACAGATGCGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTGAC	900
QY	962	TTTTGAGGAGGTTGTTCATCATGATCACAACAGAAGAACGGGCTCGTTTATCCACAGTGA	1021
Db	901	TTTTGAGGAGGTTGTTCATCATGATCACAACAGAAGAACGGGCTCGTTTATCCACAGTGA	960
QY	1022	GGAGCAGGACGCTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCATCCCTTC	1081
Db	961	GGAGCAGGACGCTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCATCCCTTC	1020
QY	1082	TTTCAAAAAGGGATCCTTTTCATAGAGAACACACTGAGAGATTACTTGAAGATTTTGATTT	1141
Db	1021	TTTCAAAAAGGGATCCTTTTCATAGAGAACACACTGAGAGATTACTTGAAGATTTTGATTT	1080
QY	1142	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAAATAGGTAAA	1201
Db	1081	CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAAATAGGTAAA	1140
QY	1202	AGTAGTCTCTAACTTCCAGGCCCCAGGCTCAGTGAATTGGAATTAAGTCTGCAATTTACAGTG	1261
Db	1141	AGTAGTCTCTAACTTCCAGGCCCCAGGCTCAGTGAATTGGAATTAAGTCTGCAATTTACAGTG	1200
QY	1262	TAGAGTAACACATAACTTGTATGCATGGAACATGAGGAACAGTATTACAGTGTCCTA	1321
Db	1201	TAGAGTAACACATAACTTGTATGCATGGAACATGAGGAACAGTATTACAGTGTCCTA	1260
QY	1322	CCACTCTAATCAAGAAAAAAGAAATTACAGACTGCTGATTTCTACAGTGATGATTTGAAATCTAAA	1381
Db	1261	CCACTCTAATCAAGAAAAAAGAAATTACAGACTGCTGATTTCTACAGTGATGATTTGAAATCTAAA	1320
QY	1382	AATGCTTATCATTAGGGCTTTTGATTTATATAAACTTTGGGTACTTATACTAATAATTATGCT	1441
Db	1321	AATGCTTATCATTAGGGCTTTTGATTTATATAAACTTTGGGTACTTATACTAATAATTATGCT	1380
QY	1442	AGTTATTTCTGCCCTCCAGTTTGCCTTGATATATTGTTGATATTAAAGATTCTTGACTTATA	1501
Db	1381	AGTTATTTCTGCCCTCCAGTTTGCCTTGATATATTGTTGATATTAAAGATTCTTGACTTATA	1440
QY	1502	TTTTGAATGGGTTCTAGTGA AAAAAGGAATGATATATTCTTGAAGACATCGATATACATTTT	1561
Db	1441	TTTTGAATGGGTTCTAGTGA AAAAAGGAATGATATATTCTTGAAGACATCGATATACATTTT	1500
QY	1562	ATTTAACACTCTTGAATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT	1621
Db	1501	ATTTAACACTCTTGAATTTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT	1560
QY	1622	AAAAGTCACGTGAACAGA 1640	
Db	1561	AAAAGTCACGTGAACAGA 1579	
RESULT 13			
AAA06347			
ID	AAA06347 standard; cDNA; 1621 BP.		
AC	AAA06347;		
XX			
DT	13-JUN-2000 (first entry)		
XX			

|||||
 Db 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCCGCGTT 360
 QY 422 AGCTGGCCACGATATCACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGGCAGAAG 481
 Db 361 AGCTGGCCACGATATCACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGGCAGAAG 420
 QY 482 TGGTGAGAATCCGTATGCCCGCCGCTGAATCTCCGTGACTTTGCTGGTGGGCGCTTAT 541
 Db 421 TGGTGAGAATCCGTATGCCCGCCGCTGAATCTCCGTGACTTTGCTGGTGGGCGCTTAT 480
 QY 542 GTGTGCACCTGGGCATTAATAATGGCTCTTTTGGACCCGACACAGCAGCTGGCAAGGTCAGGT 601
 Db 481 GTGTGCACCTGGGCATTAATAATGGCTCTTTTGGACCCGACACAGCAGCTGGCAAGGTCAGGT 540
 QY 602 CATTGATGCAAAATATGTGGGAAGGAAGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA 661
 Db 541 CATTGATGCAAAATATGTGGGAAGGAAGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA 600
 QY 662 GAAATCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGGTGGAGACCTTT 721
 Db 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGAGACAGACATGTTGATGGTGGAGACCTTT 660
 QY 722 CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 781
 Db 661 CTATACGACTTACAGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 720
 QY 782 GTTCTACGAGCTGCTGATCAAGGACTTGACATAAGTCTGATGAACCTCCCAATCAGAT 841
 Db 721 GTTCTACGAGCTGCTGATCAAGGACTTGACATAAGTCTGATGAACCTCCCAATCAGAT 780
 QY 842 GAGCATGGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 901
 Db 781 GAGCATGGATGATGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCCAAGAAGAC 840
 QY 902 GAAGGCAGAGTGGTGTCAATCTTTGACGGGCACAGATGCCGTGTGACTCCGGTCTGAC 961
 Db 841 GAAGGCAGAGTGGTGTCAATCTTTGACGGGCACAGATGCCGTGTGACTCCGGTCTGAC 900
 QY 962 TTTTGAGAGGTTGTTCATCATGATCACAAACAAGGAGGCGCTGTTTATCACCAGTGA 1021
 Db 901 TTTTGAGAGGTTGTTCATCATGATCACAAACAAGGAGGCGCTGTTTATCACCAGTGA 960
 QY 1022 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1081
 Db 961 GGAGCAGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTC 1020
 QY 1082 TTTCAAAAGGATCCTTTTCATAGGAGAACACACACTGAGAGATACTTGAAGAAATTGGATT 1141
 Db 1021 TTTCAAAAGGATCCTTTTCATAGGAGAACACACACTGAGAGATACTTGAAGAAATTGGATT 1080
 QY 1142 CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAGGTAA 1201
 Db 1081 CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAGGTAA 1140
 QY 1202 AGCTAGTCTTAACCTTCAGGCCCCAGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1261
 Db 1141 AGCTAGTCTTAACCTTCAGGCCCCAGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1200
 QY 1262 TAGAGTAACACATACATGTATGATGGAACATGAGGAACAGTATTTACAGTGTCTTA 1321
 Db 1201 TAGAGTAACACATACATGTATGATGGAACATGAGGAACAGTATTTACAGTGTCTTA 1260
 QY 1322 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATGAATTTCTAAA 1381
 Db 1261 CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATGAATTTCTAAA 1320
 QY 1382 AATGTTATCATTAGGCTTTTGAATTTATAAACTTTGGTACTTATACTATAATTTATGTT 1441
 Db 1321 AATGTTATCATTAGGCTTTTGAATTTATAAACTTTGGTACTTATACTATAATTTATGTT 1380
 QY 1442 AGTTATTCGCTTCAGTTGCTTGATATATTTGTGATATTAAGATTTCTGACTTATA 1501
 |||||

Db 1381 AGTTATTCGCTTCACGTTTGCTTGATATATTTGTTGATATTAAGATTTCTGACTTATA 1440
 QY 1502 TTTTGAATGGTTCCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1561
 Db 1441 TTTTGAATGGTTCCTAGTGAAGAAAGAAATGATATATTTCTTGAAGACATCGATATACATTT 1500
 QY 1562 ATTTACACTCTTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGATGTTGAT 1621
 Db 1501 ATTTACACTCTTGATTTCTACATGTAGAAAATGAGAAATGCCACAATTTGATGTTGAT 1560
 QY 1622 AAAAGTCACGTGAACAGA 1640
 Db 1561 AAAAGTCACGTGAACAGAA 1579
 RESULT 14
 AAS63555
 ID AAS63555 standard; cDNA; 1621 BP.
 XX
 AC AAS63555;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA sequence #107.
 XX
 KW Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI: 2001-639232/73.
 DR P-PSDB; AAU69761.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 XX
 PS Claim 1; Page 264-265; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.

XX	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;	
XX	Query Match	78.5%; Score 1574.2; DB 22; Length 1621;
XX	Best Local Similarity	99.8%; Pred. No. 0;
XX	Matches 1576; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	62 CGCCATGGCACTGCAGAGGCATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGGCCGCTT	121
Db	1 CGCCATGGCACTGCAGAGGCATCTCGGTCATGAGCTGTCCGGCCCTGGCCCCGGGCCGCTT	60
QY	122 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGGTGTGGTACGCGGTGGACCGGGCGGCTC	181
Db	61 CTGTGCTATGGTCTCTGGCTGACTTCGGGGCGCGGTGTGGTACGCGGTGGACCGGGCGGCTC	120
QY	182 CCGCTACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGAGACCTGAAGCA	241
Db	121 CCGCTACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTGTGAGACCTGAAGCA	180
QY	242 GCCGGGGGAGCCCGCGCTGCTGGCGGCTGTGCAAGCGGTCGGATGTGCTGTGAGCC	301
Db	181 GCCGGGGGAGCCCGCGCTGCTGGCGGCTGTGCAAGCGGTCGGATGTGCTGTGAGCC	240
QY	302 CTTCGGCGCGGCTGTCAATGAGAAACCTCAGCTGGGCCAGAGATTCTGCAGCGGAAAA	361
Db	241 CTTCGGCGCGGCTGTCAATGAGAAACCTCAGCTGGGCCAGAGATTCTGCAGCGGAAAA	300
QY	362 TCCAAGGCTTATTTATGCGCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTT	421
Db	301 TCCAAGGCTTATTTATGCGCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTT	360
QY	422 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGGTCTCTCAAAAATTGGCAGAG	481
Db	361 AGCTGGCCACGATATCAACTATTGGCTTTGTACAGGTCTCTCAAAAATTGGCAGAG	420
QY	482 TGGTGAAGATCCGTATGCCCCGCTGAATCTCTGGCTGACTTGTGCTGTGGCCCTTAT	541
Db	421 TGGTGAAGATCCGTATGCCCCGCTGAATCTCTGGCTGACTTGTGCTGTGGCCCTTAT	480
QY	542 GTGTGCACTGGGCATTTATATGGCTTTTGTACCGGCACACGCACTGGCAAGGTCAGGT	601
Db	481 GTGTGCACTGGGCATTTATATGGCTTTTGTACCGGCACACGCACTGGCAAGGTCAGGT	540
QY	602 CATTGATGCAATATGTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA	661
Db	541 CATTGATGCAATATGTGGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACTCA	600
QY	662 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGATGGTGGAGCACCTTT	721
Db	601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGATGGTGGAGCACCTTT	660
QY	722 CTATACGACTTACAGGACAGCAGATGGGGAATTCAATGGCTGTGGAGCAATAGAACCCA	781
Db	661 CTATACGACTTACAGGACAGCAGATGGGGAATTCAATGGCTGTGGAGCAATAGAACCCA	720
QY	782 GTTCTACGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCCCAATCAGAT	841
Db	721 GTTCTACGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCCCAATCAGAT	780
QY	842 GAGCATGATGATGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCAAGAAGAC	901
Db	781 GAGCATGATGATGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCAAGAAGAC	840
QY	902 GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGAC	961
Db	841 GAAGCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGAC	900
QY	962 TTTTGAGAGGTTGTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA	1021
Db	901 TTTTGAGAGGTTGTTCATCATGATCACAACAAGAACGGGGCTCGTTTATCACCAGTGA	960
QY	1022 GGAGCAGAGCTGAGCCCCCGCCTGCACCTCTGCTTAAACACCCAGCCATCCCTTC	1081

Db	961 GGAGCAGAGCTGAGCCCCCGCCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTC	1020
QY	1082 TTTCAAAGGATCTTTTCATAGAGAAACACACTGAGAGATATCTGAAGAATTTGCATT	1141
Db	1021 TTTCAAAGGATCTTTTCATAGAGAAACACACTGAGAGATATCTGAAGAATTTGCATT	1080
QY	1142 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAATAGGTAA	1201
Db	1081 CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAATCATTTGAAGTAATAGGTAA	1140
QY	1202 AGCTAGTCTTAACCTTCCAGGCCACGGCTCAAGTGAATTTGAATTACTGCATTTACAGTG	1261
Db	1141 AGCTAGTCTTAACCTTCCAGGCCACGGCTCAAGTGAATTTGAATTACTGCATTTACAGTG	1200
QY	1262 TAGAGTAACACATTAATGTTGATGCATGGAACACATGGAAGAACAGTATTACAGTGTCTA	1321
Db	1201 TAGAGTAACACATTAATGTTGATGCATGGAACACATGGAAGAACAGTATTACAGTGTCTA	1260
QY	1322 CCACCTAATCAAGAAAGAATTAACAGACTCTGATTTCTACAGTGAATGATGTAATCTAAA	1381
Db	1261 CCACCTAATCAAGAAAGAATTAACAGACTCTGATTTCTACAGTGAATGATGTAATCTAAA	1320
QY	1382 AATGTTATCATTAAGGCTTTTGAATTTATAAAACCTTTGGTACTTATTAATAATATGCT	1441
Db	1321 AATGTTATCATTAAGGCTTTTGAATTTATAAAACCTTTGGTACTTATTAATAATATGCT	1380
QY	1442 AGTTATTTCTGCCCTTCCAGTTTGGCTGATATATTGTTGATATTAGATTCTTGACTTATA	1501
Db	1381 AGTTATTTCTGCCCTTCCAGTTTGGCTGATATATTGTTGATATTAGATTCTTGACTTATA	1440
QY	1502 TTTTGAATGGGTTAGTGAAAAAGAAATGATATATCTTGAAGACATCGATATACATTT	1561
Db	1441 TTTTGAATGGGTTAGTGAAAAAGAAATGATATATCTTGAAGACATCGATATACATTT	1500
QY	1562 ATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGGAAATGCCACAATTTGTATGTTGAT	1621
Db	1501 ATTTACACTCTTGATTTCTACAATGTAGAAAAATGAGGAAATGCCACAATTTGTATGTTGAT	1560
QY	1622 AAAAGTCACGTGAACAGA 1640	
Db	1561 AAAAGTCACGTGAACAAA 1579	
RESULT 15		
AAS10106		
ID	AAS10106 standard; cDNA; 1621 BP.	
XX	AAS10106;	
AC	XX	
XX	XX	
DT	24-OCT-2001 (first entry)	
DE	Human prostate tumour cDNA F1-12 #3.	
XX	XX	
KW	Human; prostate tumour protein; prostate cancer; ss.	
OS	Homo sapiens.	
PN	US6262245-B1.	
XX	XX	
PD	17-JUL-2001.	
XX	XX	
PF	25-FEB-1998; 98US-0030607.	
XX	XX	
PR	25-FEB-1997; 97US-080609.	
PR	01-AUG-1997; 97US-0904804.	
PR	09-FEB-1998; 98US-0020956.	
XX	XX	
PA	(CORI-) CORIXA CORP.	
XX	XX	
PI	Xu J, Dillon DC;	
XX	XX	
DR	WPI; 2001-440862/47.	
DR	P-PSDB; AAU04959.	

XX	Novel polynucleotide encoding polypeptide comprising a portion of
PT	prostate tumour protein useful for inhibiting development of prostate
PT	cancer or for treating prostate cancer in a patient
XX	
XX	
PS	Claim 1; Column 112-113; 105pp; English.
XX	
CC	The sequence is a human prostate tumour cDNA which encodes a
CC	partial tumour protein. The DNA is useful for inhibiting the development
CC	of prostate cancer or for treating prostate cancer in a patient.
XX	
SO	Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 other;

Query Match	78.58;	Score 1574.2;	DB 22;	Length 1621;
Best Local Similarity	99.88;	Pred. No. 0;		
Matches 1576; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	62	CGCCATGGCACTGCAGGGCAATCTCGGTCTGTGAGCTGTCCGGCTGGCCCCGGCCGTT	121
Db	1	CGCCATGGCACTGCAGGGCAATCTCGGTCTGTGAGCTGTCCGGCTGGCCCCGGCCGTT	60
QY	122	CTGTGCTATGTCCTGGCTGACTTCGGGGCCGCTGTGGTACCCGTGACCGCGCCGCTC	181
Db	61	CTGTGCTATGTCCTGGCTGACTTCGGGGCCGCTGTGGTACCCGTGACCGCGCCGCTC	120
QY	182	CCGCTACGACGTGAGCCCGCTTGGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA	241
Db	121	CCGCTACGACGTGAGCCCGCTTGGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCA	180
QY	242	GCCGGGGGAGCCCGCTGTCTCGGGCGTCTGTGCAAGCGTCCGATGTCTGTGAGCC	301
Db	181	GCCGGGGGAGCCCGCTGTCTCGGGCGTCTGTGCAAGCGTCCGATGTCTGTGAGCC	240
QY	302	CTTCCGCCCGCGGTGCATGTGAGAACTCCAGCTGGCCACAGATTCAGCGGGGAAA	361
Db	241	CTTCCGCCCGCGGTGCATGTGAGAACTCCAGCTGGCCACAGATTCAGCGGGGAAA	300
QY	362	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGAGAAGCTTCTGCCGTT	421
Db	301	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGAGAAGCTTCTGCCGTT	360
QY	422	AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAG	481
Db	361	AGCTGGCCACGATATCAACTATTGGCTTTGTCAAGGTGTTCTCTCAAAAATTGGCAGAAG	420
QY	482	TGGTGAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGTGGCCTTAT	541
Db	421	TGGTGAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGTGTGGCCTTAT	480
QY	542	GTTGTCACTGGGCATTAATAAGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGT	601
Db	481	GTTGTCACTGGGCATTAATAAGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGT	540
QY	602	CATTGATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCA	661
Db	541	CATTGATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCA	600
QY	662	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGTTGAGACCACTTT	721
Db	601	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGACATGTTGGATGTTGAGACCACTTT	660
QY	722	CTATACGACTTACAGGACAGACAGATGGGGAAATTCATGCGCTGTTGAGCAATAGAACCCCA	781
Db	661	CTATACGACTTACAGGACAGACAGATGGGGAAATTCATGCGCTGTTGAGCAATAGAACCCCA	720
QY	782	GTTCTACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAATTCCCAATCAGAT	841
Db	721	GTTCTACGAGCTGCTGATCAAAAGCACTTGGACTAAAGTCTGATGAATTCCCAATCAGAT	780
QY	842	GAGCATGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCCAAAAGAAGAC	901
Db	781	GAGCATGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCCAAAAGAAGAC	840

QY	902	GAAGGCAGAGTGGTGTCTCAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGTAC	961
Db	841	GAAGGCAGAGTGGTGTCTCAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGTAC	900
QY	962	TTTTGAGGAGGTGTTCATCATGTATCACACAAGGAACGGGGCTGTTATCACCAGTGA	1021
Db	901	TTTTGAGGAGGTGTTCATCATGTATCACACAAGGAACGGGGCTGTTATCACCAGTGA	960
QY	1022	GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTTTAAACCCAGCCATCCCTTC	1081
Db	961	GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTTTAAACCCAGCCATCCCTTC	1020
QY	1082	TTTCAAAAGGATCCTTTCATAGGAGAACAACACACTGAGGAGATCTTGAAGATTTGGATT	1141
Db	1021	TTTCAAAAGGATCCTTTCATAGGAGAACAACACACTGAGGAGATCTTGAAGATTTGGATT	1080
QY	1142	CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAGGTAAA	1201
Db	1081	CAGCCGCGAAGAGATTTATCAGCTTAACCTCAGATAAATCATTTGAAGTAATAGGTAAA	1140
QY	1202	AGCTAGTCTCTAAGTCTCCAGCGCCACGGCTCAAGTGAATTTGAATCTGCATTTACAGTG	1261
Db	1141	AGCTAGTCTCTAAGTCTCCAGCGCCACGGCTCAAGTGAATTTGAATCTGCATTTACAGTG	1200
QY	1262	TAGAGTAACACATTAACATTTATATGCATGGAACATGAGGAACAGTATTACAGTGTCTTA	1321
Db	1201	TAGAGTAACACATTAACATTTATATGCATGGAACATGAGGAACAGTATTACAGTGTCTTA	1260
QY	1322	CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATTTGAATTCFAAA	1381
Db	1261	CCACTCTAATCAAGAAAGAATTACAGACTCTGATTTCTACAGTATGATTTGAATTCFAAA	1320
QY	1382	AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATCTAAATTATGGT	1441
Db	1321	AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATCTAAATTATGGT	1380
QY	1442	AGTTATTTCTGCCCTCCAGTTTGCTTGATATATTTGTTGATATTAGATTTCTTGACTTATA	1501
Db	1381	AGTTATTTCTGCCCTCCAGTTTGCTTGATATATTTGTTGATATTAGATTTCTTGACTTATA	1440
QY	1502	TTTTGAATGGGTCTAGTGAAGGAATGATATATTCTTGAAGACATCGATATACATTT	1561
Db	1441	TTTTGAATGGGTCTAGTGAAGGAATGATATATTCTTGAAGACATCGATATACATTT	1500
QY	1562	ATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAATTTGTATGGTAT	1621
Db	1501	ATTTACACTCTTGATTTCTACAATGTAGAAATGAGGAATGCCACAATTTGTATGGTAT	1560
QY	1622	AAAAGTCACGTGAACACAGA 1640	
Db	1561	AAAAGTCACGTGAACACAAA 1579	

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